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OM protein - protein search, using sw model

Run on: May 30, 2006, 15:08:01 ; Search time 19.333 Seconds  
(without alignments)  
81.494 Million cell updates/sec

Title: US-10-758-165A-10  
Perfect score: 97  
Sequence: 1 VDCQKATNIPYTPAKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 271358

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /EMC\_Celerra\_SIDS3/prodata/2/iaa/5.COMB.pep.\*  
2: /EMC\_Celerra\_SIDS3/prodata/2/iaa/6.COMB.pep.\*  
3: /EMC\_Celerra\_SIDS3/prodata/2/iaa/7.COMB.pep.\*  
4: /EMC\_Celerra\_SIDS3/prodata/2/iaa/H.COMB.pep.\*  
5: /EMC\_Celerra\_SIDS3/prodata/2/iaa/PCUS.COMB.pep.\*  
6: /EMC\_Celerra\_SIDS3/prodata/2/iaa/RE.COMB.pep.\*  
7: /EMC\_Celerra\_SIDS3/prodata/2/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	33.0	9	2	US-09-920-262A-6
2	32	33.0	15	2	US-09-674-973A-64
3	31	32.0	11	2	US-09-307-265A-14
4	31	32.0	12	1	US-08-260-582-47
5	31	32.0	12	1	US-08-260-582-48
6	31	32.0	12	5	PCT-US95-05471-47
7	31	32.0	12	5	PCT-US95-05471-48
8	30	30.9	9	2	US-09-865-548A-126
9	30	30.9	14	2	US-09-502-426B-27
10	30	30.9	17	1	US-08-333-565-22
11	30	30.9	17	1	US-08-661-479-22
12	29	29.9	9	2	US-09-042-353-366
13	29	29.9	9	2	US-08-758-417A-214
14	29	29.9	15	2	US-08-278-774-20
15	29	29.9	18	2	US-09-856-920-1
16	28	28.9	10	2	US-09-641-803-18
17	28	28.9	10	2	US-09-641-802-18
18	28	28.9	10	2	US-09-641-801-18
19	28	28.9	10	2	US-10-281-652-18
20	28	28.9	11	1	US-07-958-903A-10
21	28	28.9	11	1	US-08-462-018-10
22	28	28.9	11	1	US-08-823-245-10
23	28	28.9	11	2	US-07-963-329A-60
24	28	28.9	11	2	US-09-318-001-10
25	28	28.9	11	2	US-09-064-159-10
26	28	28.9	11	5	PCT-US92-09443A-60

27	28	28.9	15	1	US-08-080-073-26	Sequence 26, Appl
28	28	28.9	16	2	US-10-044-708A-3	Sequence 3, Appl
29	28	28.9	18	1	US-08-084-718-30	Sequence 30, Appl
30	28	28.9	18	1	US-08-443-976-30	Sequence 30, Appl
31	28	28.9	11	2	US-09-809-517A-21	Sequence 21, Appl
32	27	27.8	18	1	US-08-421-702A-100	Sequence 100, Appl
33	27	27.8	18	1	US-08-303-052A-100	Sequence 100, Appl
34	27	27.8	18	1	US-08-421-696A-100	Sequence 100, Appl
35	27	27.8	18	1	US-08-421-697A-100	Sequence 100, Appl
36	27	27.8	18	1	US-08-421-698A-100	Sequence 100, Appl
37	27	27.8	18	1	US-08-421-699A-100	Sequence 100, Appl
38	27	27.8	18	1	US-08-421-700A-100	Sequence 100, Appl
39	27	27.8	18	1	US-08-421-701A-100	Sequence 100, Appl
40	27	27.8	18	1	US-08-421-702A-100	Sequence 100, Appl
41	26	26.8	5	2	US-09-768-006-9	Sequence 9, Appl
42	26	26.8	8	3	US-09-641-528B-1718	Sequence 1718, Ap
43	26	26.8	8	3	US-09-641-528B-8847	Sequence 8847, Ap
44	26	26.8	8	3	US-09-641-528B-16358	Sequence 16358, A
45	26	26.8	8	3	US-09-641-528B-23996	Sequence 23996, A

ALIGNMENTS

RESULT 1  
US-09-920-262A-6  
; Sequence 6, Application US/09920262A  
; Patent No. 6902734  
; GENERAL INFORMATION:  
; APPLICANT: Shealy, David  
; APPLICANT: Knight, David  
; APPLICANT: Scallion, Bernie  
; APPLICANT: Giles-Komar, Jill  
; APPLICANT: Peritt, David  
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES  
; FILE REFERENCE: CEN0248  
; CURRENT APPLICATION NUMBER: US/09/920, 262A  
; PRIOR FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: 60/223,358  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: 60/236,827  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver 3.1  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-920-262A-6  
Query Match 33.0%; Score 32; DB 2; Length 9;  
Best Local Similarity 83.3%; Pred. No. 5e+05;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 8 NIPYPT 13  
Db 4 NIPYPT 9  
RESULT 2  
US-09-674-973A-64  
; Sequence 64, Application US/09674973A  
; Patent No. 6759046  
; GENERAL INFORMATION:  
; APPLICANT: No. 6759046sk Hydro ASA  
; TITLE OF INVENTION: Peptides  
; FILE REFERENCE: 26625-296  
; CURRENT APPLICATION NUMBER: US/09/674, 973A  
; CURRENT FILING DATE: 2001-06-04  
; NUMBER OF SEQ ID NOS: 459  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 64  
; LENGTH: 15

TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-674-973A-64

Query Match 33.0%; Score 31; DB 2; Length 15;  
Best Local Similarity 54.5%; Pred. No. 1e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VDGGKATNIFP 11  
|:|:|:|:  
Db 4 VEDOKTIVFP 14

RESULT 3  
US-09-307-265A-14  
Sequence 14, Application US/09307265A  
Patent No. 6223456  
GENERAL INFORMATION:  
APPLICANT: Gu, Trent  
APPLICANT: Oxita, Satoshi  
APPLICANT: Han, Min  
TITLE OF INVENTION: RAS SUPPRESSOR SUR-5  
FILE REFERENCE: UTC-03732  
CURRENT APPLICATION NUMBER: US/09/307,265A  
CURRENT FILING DATE: 1999-05-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 14  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Caenorhabditis elegans  
US-09-307-265A-14

Query Match 32.0%; Score 31; DB 2; Length 11;  
Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 11 PYTAGKQ 18  
|:|:|:|:  
Db 1 PYTSSGKK 8

RESULT 4  
US-08-260-582-47  
Sequence 47, Application US/08260582  
Patent No. 5635182  
GENERAL INFORMATION:  
APPLICANT: McCoy, John M.  
APPLICANT: Lu, Zhifan  
TITLE OF INVENTION: METHOD OF DETECTING LIGAND  
TITLE OF INVENTION: INTERACTIONS  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: U.S.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/260,582  
FILING DATE: 16-JUN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiner, M. C.  
REGISTRATION NUMBER: 31,544  
REFERENCE/DOCKET NUMBER: GI 5236  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 876-1170  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-260-582-47

Query Match 32.0%; Score 31; DB 1; Length 12;  
Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 11 PYTAGKQ 18  
|:|:|:|:  
Db 4 PWLAPGQ 11

RESULT 5  
US-08-260-582-48  
Sequence 48, Application US/08260582  
Patent No. 5635182  
GENERAL INFORMATION:  
APPLICANT: McCoy, John M.  
APPLICANT: Lu, Zhifan  
TITLE OF INVENTION: METHOD OF DETECTING LIGAND  
TITLE OF INVENTION: INTERACTIONS  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: U.S.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/260,582  
FILING DATE: 16-JUN-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Meiner, M. C.  
REGISTRATION NUMBER: 31,544  
REFERENCE/DOCKET NUMBER: GI 5236  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 876-1170  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 48:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-260-582-48

Query Match 32.0%; Score 31; DB 1; Length 12;  
Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 11 PYTAGKQ 18  
|:|:|:|:  
Db 4 PWLAPGQ 11

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RESULT 6
PCT-US95-05471-47
; Sequence 47, Application PC/TUS9505471
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: METHOD OF DETECTING LIGAND INTERACTIONS
; NUMBER OF SEQUENCES: 76
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05471
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEITICAL: NO
; ANTI-SENSE: NO
PCT-US95-05471-47

Query Match          32.0%; Score 31; DB 5; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy      11 PYTAPGKQ 18
      |||
      4 PWLAPGEQ 11

RESULT 7
PCT-US95-05471-48
; Sequence 48, Application PC/TUS9505471
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: METHOD OF DETECTING LIGAND INTERACTIONS
; NUMBER OF SEQUENCES: 76
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05471
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEITICAL: NO
; ANTI-SENSE: NO
PCT-US95-05471-48

Query Match          32.0%; Score 31; DB 5; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy      11 PYTAPGKQ 18
      |||
      4 PWLAPGEQ 11

RESULT 8
US-09-865-548A-126
; Sequence 126, Application US/09865548A
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Patent No. 6867283
; GENERAL INFORMATION:
; APPLICANT: Barnea, Elion
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamara
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865, 548A
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 126
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-126

Query Match          30.9%; Score 30; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      8 NIPFY 12
      |||
      1 NIPFY 5

RESULT 9
US-09-502-426B-27
; Sequence 27, Application US/09502426B
; Patent No. 6987025
; GENERAL INFORMATION:
; APPLICANT: Azpiroz, Ricardo
; APPLICANT: Choe, Sungna
; APPLICANT: Feldmann, Kenneth A.
; TITLE OF INVENTION: DMF4 POLYNUCLEOTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 11696-070001
; CURRENT APPLICATION NUMBER: US/09/502,426B
; CURRENT FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/119,657
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: US 60/119,658
; PRIOR FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heme binding domain
US-09-502-426B-27

Query Match          30.9%; Score 30; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy      10 PPYAPGKQ 18
      |||
      5 PPRLCPGKE 13

RESULT 10
US-08-333-565-22
; Sequence 22, Application US/08333565
; Patent No. 5622852
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
```

TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
TITLE OF INVENTION: REGULATOR  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/333,565  
FILING DATE: 31-OCT-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000700  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-333-565-22

Query Match 30.9%; Score 30; DB 1; Length 17;  
Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 PYTAG 16  
Db 3 PYLAG 8

RESULT 11  
US-08-661-479-22  
Sequence 22, Application US/08661479  
Patent No. 5834209  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
TITLE OF INVENTION: REGULATOR  
NUMBER OF SEQUENCES: 59  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/661,479  
FILING DATE: 11-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/333,565  
FILING DATE: 31-OCT-1994  
ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 15726A-000700  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-661-479-22

Query Match 30.9%; Score 30; DB 1; Length 17;  
Best Local Similarity 83.3%; Pred. No. 2.5e+02;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 PYTAG 16  
Db 3 PYLAG 8

RESULT 12  
US-09-042-353-366  
Sequence 366, Application US/09042353  
Patent No. 6255458  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for  
Producing Heterologous Antibodies  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 421  
CORRESPONDENCE ADDRESSES:  
ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,353  
FILING DATE: 13-MAR-1998  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/161,739



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      FILING DATE: 03-DEC-1993
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/165,699
      FILING DATE: 10-DEC-1993
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/209,741
      FILING DATE: 09-MAR-1994
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/352,322
      FILING DATE: 07-DEC-1994
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/544,404
      FILING DATE: 10-OCT-1995
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/728,463
      FILING DATE: 10-OCT-1996
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: WO PCT/US96/16433
      FILING DATE: 10-OCT-1996
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/758,417
      FILING DATE: 02-DEC-1996
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: WO PCT/US97/21803
      FILING DATE: 01-DEC-1997
      ATTORNEY/AGENT INFORMATION:
      NAME: Apple, Randolph T.
      REGISTRATION NUMBER: 36,429
      REFERENCE/DOCKET NUMBER: 014643-009040US
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (415) 576-0200
      TELEFAX: (415) 576-0300
      INFORMATION FOR SEQ ID NO: 366:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 9 amino acids
      TYPE: amino acid
      STRANDEDNESS:
      TOPOLOGY: linear
      MOLECULE TYPE: peptide
      US-09-042-353-366

Query Match      29.9% Score 29; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. Se+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 NIPYT 13
      1
      4 NSFPYT 9

RESULT 13
US-08-758-417A-214
; Sequence 214, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 417
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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      APPLICATION NUMBER: US/08/758,417A
      FILING DATE: 02-DEC-1996
      CLASSIFICATION: <Unknown>
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/728,463
      FILING DATE: 10-OCT-1996
      APPLICATION NUMBER: US 08/544,404
      FILING DATE: 10-OCT-1995
      APPLICATION NUMBER: US 08/352,322
      FILING DATE: 07-DEC-1994
      APPLICATION NUMBER: US 08/209,741
      FILING DATE: 09-MAR-1994
      APPLICATION NUMBER: US 08/165,699
      FILING DATE: 10-DEC-1993
      APPLICATION NUMBER: US 08/161,739
      FILING DATE: 03-DEC-1993
      APPLICATION NUMBER: US 08/155,301
      FILING DATE: 18-NOV-1993
      APPLICATION NUMBER: US 08/096,762
      FILING DATE: 22-JUL-1993
      APPLICATION NUMBER: US 08/053,131
      FILING DATE: 26-APR-1993
      APPLICATION NUMBER: US 07/990,860
      FILING DATE: 16-DEC-1992
      ATTORNEY/AGENT INFORMATION:
      NAME: Serafini, Andrew T.
      REGISTRATION NUMBER: 41,303
      REFERENCE/DOCKET NUMBER: 014643-009030US
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (415) 576-0200
      TELEFAX: (415) 576-0300
      INFORMATION FOR SEQ ID NO: 214:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 9 amino acids
      TYPE: amino acid
      STRANDEDNESS: <Unknown>
      TOPOLOGY: linear
      MOLECULE TYPE: peptide
      SEQUENCE DESCRIPTION: SEQ ID NO: 214:

US-08-758-417A-214

Query Match      29.9% Score 29; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. Se+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 NIPYT 13
      1
      4 NSFPYT 9

RESULT 14
US-08-278-774-20
; Sequence 20, Application US/08278774
; Patent No. 6653450
; GENERAL INFORMATION:
; APPLICANT: Berg, Richard A
; Applicant: Tomam, David P
; APPLICANT: Wallace, Donald
; TITLE OF INVENTION: MUTATED RECOMBINANT COLLAGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: COLLAGEN CORPORATION
; STREET: 2500 Faber Place
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```

```

; APPLICATION NUMBER: US/08/278,774
; FILING DATE: 22-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Katalyxo, Kachi L
; REGISTRATION NUMBER: 36,644
; REFERENCE/DOCKET NUMBER: 94-018
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 354-4642
; TELEFAX: (415) 354-4752
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-278-774-20

```

```

Query Match          29.9%; Score 29; DB 2; Length 15;
Best Local Similarity 41.7%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

```

```

Qy      1 VDGQKATNIFPY 12
       :|:|:|:|
Db      2 IGGEKAGGPAPY 13

```

```

RESULT 15
US-09-856-920-1
; Sequence 1, Application US/09856920
; Patent No. 6740325
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co.
; TITLE OF INVENTION: Peptide-based vaccine for influenza
; FILE REFERENCE: 9822 PCT
; CURRENT APPLICATION NUMBER: US/09/856,920
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Influenza virus
US-09-856-920-1

```

```

Query Match          29.9%; Score 29; DB 2; Length 18;
Best Local Similarity 44.4%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Qy      7 TNIFPYTAP 15
       :|:|:|:|
Db      5 SNCYPTDVP 13

```

```

Search completed: May 30, 2006, 15:09:26
Job time : 20.333 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

# OM protein - protein search, using sw model

Run on: May 30, 2006, 15:04:28 ; Search time 12 Seconds  
(without alignments)  
144.325 Million cell updates/sec

Title: US-10-758-165A-11  
Perfect score: 96  
Sequence: 1 IDGQKVDPPQHGVLKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*  
1: Dirl:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	26.0	14	2	A56632 neosulfakinin-II -
2	24	25.0	15	2	PT0090 alpha-glucosidase
3	24	25.0	18	2	A61577 24k serine protein
4	23	24.0	11	1	GMROL leucosulfakinin -
5	23	24.0	11	2	A60656 perisulfakinin - A
6	23	24.0	16	2	D96655 T-cell-receptor be
7	23	24.0	16	2	C90981 his operon leader
8	23	24.0	16	2	A65827 his operon leader
9	23	24.0	18	2	S70340 napin large chain
10	22	22.9	9	2	B39841 dextranucrase (EC
11	22	22.9	11	2	A33917 dihydroorotase (EC
12	22	22.9	18	2	S29379 sorbitol dehydroge
13	21	21.9	7	2	A34818 vitellin 72K chain
14	21	21.9	14	2	PC7075 guanylate cyclase
15	21	21.9	15	2	A30330 neuropeptide pep -
16	21	21.9	16	2	A49226 major outer membra
17	21	21.9	17	2	A65274 glutathione S-tran
18	21	21.9	17	2	G85956 hypothetical prote
19	21	21.9	18	2	I55453 zinc finger homeod
20	21	21.9	18	2	H75063 hypothetical prote
21	20	20.8	10	2	S33844 alpha-2-macroglobu
22	20	20.8	10	2	I48778 small nuclear ribo
23	20	20.8	10	2	G60589 sperm-activating p
24	20	20.8	12	2	G68402 NAD(+)-glycohydrol
25	20	20.8	12	2	S68271 major urinary prot
26	20	20.8	12	2	PM0170 alcohol dehydrogen
27	20	20.8	13	2	S23640 Ig kappa chain J s
28	20	20.8	13	2	S47357 T-cell antigen rec
29	20	20.8	13	2	S47358 T-cell antigen rec

30	20	20.8	14	2	PC4382 dehydrin 4.5K poly
31	20	20.8	14	2	P00152 18k iron-sulfur pr
32	20	20.8	15	2	S51735 T-cell receptor be
33	20	20.8	15	2	B49655 T-cell-receptor be
34	20	20.8	15	2	PH0789 T-cell receptor al
35	20	20.8	15	2	S71306 heat shock protein
36	20	20.8	16	2	B49255 T-cell receptor be
37	20	20.8	16	2	F49039 T-cell receptor be
38	20	20.8	18	2	D49570 plasma membrane ca
39	19.5	20.3	17	2	B36727 cytochrome c554 -
40	19	19.8	11	2	A40693 transgelin - sheep
41	19	19.8	11	2	PC2173 triacylglycerol 11
42	19	19.8	11	2	J02307 hypothetical 1.5K
43	19	19.8	14	2	C35141 T-cell receptor de
44	19	19.8	14	2	S27140 hypothetical prote
45	19	19.8	15	2	S14749 3-dehydroquinase -

## ALIGNMENTS

```

RESULT 1
A56632
neosulfakinin-II - flesh fly (Sarcophaga bullata)
N:Alternate names: Neb-SK-II
N:Contains: neosulfakinin-I (Neb-SK-I)
C:Species: Sarcophaga bullata
C>Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: A56632
R:Fonagy, A.; Schoofs, L.; Proost, P.; Van Damme, J.; De Loof, A.
Comp. Biochem. Physiol. C 103, 135-142, 1992
A>Title: Isolation and primary structure of two sulfakinin-like peptides from the fleshf
A:Reference number: A56632; MUID:93083101; PMID:1360367
A:Accession: A56632
A:Molecule type: protein
A:Residues: 1-14 <FON>
A:Cross-references: UNIPROT:P41493; UNIPARC:UPI000013054D
A:Experimental source: heads
A>Note: sequence extracted from NCBI backbone (NCBI:120391)
C:Keywords: amidated carboxyl end; neuropeptide; sulfoprotein
F:1-14/Product: neosulfakinin-II #status experimental <NSK2>
F:6-14/Product: neosulfakinin-I #status experimental <NSK1>
F:9/Binding site: sulfate (Tyr) (covalent) #status predicted
F:14/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 26.0%; Score 25; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 6.1e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 DEQPPQHG 14
Db 3 EEQPDYDG 10

RESULT 2
PT0090
alpha-glucosidase (EC 3.2.1.20) - honeybee (fragment)
C:Species: Apis mellifera (honeybee)
C>Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004
C:Accession: PT0090
R:Kimura, A.; Takata, M.; Fukushi, Y.; Mori, H.; Matsui, H.; Chiba, S.
Biosci. Biotechnol. Biochem. 61, 1091-1098, 1997
A>Title: A catalytic amino acid and primary structure of active site in Aspergillus nige
A:Reference number: PT0090; MUID:9739878; PMID:9255970
A:Accession: PT0090
A:Molecule type: protein
A:Residues: 1-15 <KIM>
A:Cross-references: UNIPROT:Q7M3M5; UNIPARC:UPI000017BF08
C:Keywords: glycosidase; hydrolase

Query Match 25.0%; Score 24; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 9.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 IDGQKVD 7  
||| :||  
Db 2 IDGFRID 8

## RESULT 3

A:Species: Streptomyces fradiae  
C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004  
C:Accession: A61577  
R:Sinha, U.; Wolz, S.A.; Iad, P.J.  
Int. J. Biochem. 23, 979-984, 1991  
A:Title: Two new extracellular serine proteases from Streptomyces fradiae.  
A:Reference number: A61577; PMID:92155439; PMID:1786859  
A:Accession: A61577  
A:Molecule type: protein  
A:Residues: 1-18 <SIN>  
A:Cross-references: UNIPROT:Q7M198; UNIPARC:UPI000017AE13  
C:Keywords: extracellular protein; hydrolase; serine protease

Query Match 25.0%; Score 24; DB 2; Length 18;  
Best Local Similarity 27.3%; Pred. No. 1.2e+03;  
Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 IDGQKVDGFP 11  
:|:|:  
Db 2 VGGTRAAQDFP 12

## RESULT 4

leucosulfakinin - Madeira cockroach  
N:Alternate names: LSK  
C:Species: Leucophaea maderae (Madeira cockroach)  
C:Date: 17-Mar-1997 #sequence\_revision 17-Mar-1987 #text\_change 09-Jul-2004  
C:Accession: A01622  
R:Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.  
Science 234, 71-73, 1986  
A:Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and ch  
A:Reference number: A01622; PMID:86315858; PMID:3749893  
A:Accession: A01622  
A:Molecule type: protein  
A:Residues: 1-11 <NAC>  
A:Cross-references: UNIPROT:P04428; UNIPARC:UPI000012E960  
C:Superfamily: gastrin  
C:Keywords: amidated carboxyl end; hormone; sulfoprotein  
F/6/Binding site: sulfate (Tyr) (covalent) #status experimental  
F/11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 24.0%; Score 23; DB 1; Length 11;  
Best Local Similarity 57.1%; Pred. No. 1e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 EQFPONG 14  
||| :|  
Db 1 EQFEDYG 7

## RESULT 5

perisulfakinin - American cockroach  
A:Species: Periplaneta americana (American cockroach)  
C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 09-Jul-2004  
C:Accession: A60656  
R:Veensira, U.A.  
Neuropeptides 14, 145-149, 1989  
A:Title: Isolation and structure of two gastrin-like neuropeptides from the American  
A:Reference number: A60656; MUID:50137190; PMID:2615921  
A:Accession: A60656  
A:Molecule type: protein  
A:Residues: 1-11 <VEE>

A:Cross-references: UNIPROT:P36885; UNIPARC:UPI000012E962  
C:Comment: This neuropeptide stimulates hindgut contractions.  
C:Keywords: amidated carboxyl end; neuropeptide; sulfoprotein  
F/6/Binding site: sulfate (Tyr) (covalent) #status experimental  
F/11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 24.0%; Score 23; DB 2; Length 11;  
Best Local Similarity 57.1%; Pred. No. 1e+03;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 EQFPONG 14  
||| :|  
Db 1 EQFDDYG 7

## RESULT 6

D49655  
T-cell-receptor beta chain variable region, TCR V beta (clone 2) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 07-Apr-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997  
C:Accession: D49655  
R:Grom, A.A.; Thompson, S.D.; Luyink, L.; Passo, M.; Choi, E.; Glaes, D.N.  
Proc. Natl. Acad. Sci. U.S.A. 90, 11104-11108, 1993  
A:Title: Dominant T-cell-receptor beta chain variable region V beta 14+ clones in juveni  
A:Reference number: A49655; MUID:94068553; PMID:8248215  
A:Accession: D49655  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-16 <GRO>  
A:Cross-references: UNIPARC:UPI000017C3CA  
A:Experimental source: peripheral blood lymphocytes  
A:Note: sequence extracted from NCBI backbone (NCBIF:140448)  
C:Keywords: T-cell receptor

Query Match 24.0%; Score 23; DB 2; Length 16;  
Best Local Similarity 55.6%; Pred. No. 1.6e+03;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 DGQKVDGFP 10  
||| :|  
Db 7 DRAPVNEQF 15

## RESULT 7

his operon leader peptide [imported] - Escherichia coli (strain O157:H7, substrain RMD  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 09-Jul-2004  
C:Accession: G90981  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kunara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom  
A:Reference number: A95629; MUID:21156231; PMID:11258796  
A:Accession: G90981  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-16 <HAY>  
A:Cross-references: UNIPROT:Q8X8T5; UNIPARC:UPI000000D08D2; GB:BA000007; PIDN:BA836242.1;  
A:Experimental source: strain O157:H7, substrain RMD 0509952  
C:Genetics:  
A:Gene: ECe2819

Query Match 24.0%; Score 23; DB 2; Length 16;  
Best Local Similarity 80.0%; Pred. No. 1.6e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 QPQKH 13  
||| :|  
Db 5 QPKQH 9

## RESULT 8

A85827  
his operon leader peptide [imported] - Escherichia coli (strain O157:H7, substrain EDL933)  
C/Species: Escherichia coli  
C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 09-Jul-2004  
C/Accession: A85827  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Mature 409, 529-533, 2001  
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A/Reference number: A85480; MUID:21074935; PMID:11206551  
A/Accession: A85827  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-16 <STO>  
A/Cross-references: UNIPROT:Q8X8T5, UNIPARC:UPI0000008D2; GB:AE005174; MID:912516199; F  
A/Experimental source: strain O157:H7, substrain EDL933  
C/Genetics:  
A/Gene: hlyE

Query Match 24.0%; Score 23; DB 2; Length 16;  
Best Local Similarity 80.0%; Pred. No. 1.6e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 QFPOH 13  
Db 5 QFPOH 9

## RESULT 9

S70340  
napin large chain L1A - Swedish turnip (fragments)  
C/Species: Brassica napus var. rapifera (Swedish turnip, rutabaga)  
C/Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 31-Dec-2004  
C/Accession: S70340  
R:Neumann, G.M.; Condron, R.; Thomas, I.; Polya, G.M.  
Biochim. Biophys. Acta 1295, 34-43, 1996  
A/Title: Purification and sequencing of multiple forms of Brassica napus seed napin larg  
A/Reference number: S70340; MUID:96283791; PMID:8676671  
A/Accession: S70340  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-12,13-18 <NEU>  
A/Cross-references: UNIPROT:Q39344; UNIPROT:Q9S9F0; UNIPARC:UPI000017B02E; UNIPARC:UPI00  
C/Superfamily: Alpha amylase inhibitor

Query Match 24.0%; Score 23; DB 2; Length 18;  
Best Local Similarity 36.4%; Pred. No. 1.8e+03;  
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 4 QKVDQFPOHG 14  
Db 1 QKVDQFPOHG 11

## RESULT 10

B39841  
dextranucrase (EC 2.4.1.5) - Streptococcus sobrinus (fragment)  
C/Species: Streptococcus sobrinus  
C/Date: 20-Mar-1992 #sequence\_revision 20-Mar-1992 #text\_change 09-Jul-2004  
C/Accession: B39841  
R:Mooser, G.; Helfa, S.A.; Paxton, R.J.; Shively, J.E.; Lee, T.D.  
J. Biol. Chem. 266, 8916-8922, 1991  
A/Title: Isolation and sequence of an active-site peptide containing a catalytic aspart  
A/Reference number: A39841; MUID:91224988; PMID:1827439  
A/Accession: B39841  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-9 <MOO>  
A/Cross-references: UNIPROT:Q7M0L7; UNIPARC:UPI000017AC69  
C/Keywords: glycosyltransferase; hexosyltransferase

Query Match 22.9%; Score 22; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 DGQKVD 7  
Db 1 DGQKVD 6

## RESULT 11

A33917  
dihydroorotase (EC 3.5.2.3) - Chinese hamster (fragment)  
C/Species: Citellulus griseus (Chinese hamster)  
C/Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 07-Nov-1997  
C/Accession: A33917  
R:Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.; Bergh, S.T.;  
Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989  
A/Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase domain and  
A/Reference number: A33917; MUID:89282776; PMID:2543974  
A/Accession: A33917  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-11 <SIM>  
A/Cross-references: UNIPARC:UPI0000176037; GB:M23652  
C/Superfamily: rudimentary enzyme; aspartate(ornithine) carbamoyltransferase homology; Bac  
arabamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-phos  
C/Keywords: hydrolase

Query Match 22.9%; Score 22; DB 2; Length 11;  
Best Local Similarity 80.0%; Pred. No. 1.5e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DGQKV 6  
Db 2 DGQKV 6

## RESULT 12

S29379  
sorbitol dehydrogenase - sheep  
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
C/Date: 19-Mar-1997 #sequence\_revision 01-Aug-1997 #text\_change 09-Jul-2004  
C/Accession: S29379  
R:Refersen, H.; Sletten, K.; McKinley-McKee, J.S.  
Eur. J. Biochem. 211, 861-869, 1993  
A/Title: Affinity labelling of sorbitol dehydrogenase from sheep liver with alpha-bromo-  
A/Reference number: S29379; MUID:93170323; PMID:8436142  
A/Accession: S29379  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-18 <RSI>  
A/Cross-references: UNIPROT:Q9TR15; UNIPARC:UPI0000087DCL  
C/Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

Query Match 22.9%; Score 22; DB 2; Length 18;  
Best Local Similarity 50.0%; Pred. No. 2.7e+03;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 7 DEQFPOHG 14  
Db 10 DVHYQHG 17

## RESULT 13

A34818  
vicillin 72K chain - pigeon pea (fragment)  
C/Species: Cajanus cajan (pigeon pea)  
C/Date: 13-Jul-1990 #sequence\_revision 13-Jul-1990 #text\_change 30-Sep-1993  
C/Accession: A34818  
R:Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.  
Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990  
A/Title: Unusual denaturation properties of vicillin from Cajanus cajan.  
A/Reference number: A34818; MUID:90165956; PMID:2306256  
A/Accession: A34818  
A/Status: preliminary

A:Molecule type: protein  
 A:Residues: 1-7 <MM>  
 A:Cross-references: UNIPARC:UPI000017BD40

Query Match 21.9%; Score 21; DB 2; Length 7;  
 Best Local Similarity 42.9%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GQKVDQ 9  
 | : || :  
 Db 1 GARVDQE 7

## RESULT 14

PC7075  
 guanylate cyclase (EC 4.6.1.2), soluble, alpha-1 chain - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C>Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 09-Jul-2004  
 C:Accession: PC7075  
 R:Taughta, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;  
 Electrophoresis 21, 1853-1871, 2000  
 A>Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of p  
 A:Reference number: PC7072  
 A:Accession: PC7075  
 A:Molecule type: protein  
 A:Residues: 1-14 <TSU>  
 A:Cross-references: UNIPROT:Q7M058; UNIPARC:UPI000017C675  
 A:Experimental source: Strain C57BL/6Ct Slc, male; brain, striatum  
 C:Keywords: brain; phosphorus-oxygen lyase

Query Match 21.9%; Score 21; DB 2; Length 14;  
 Best Local Similarity 50.0%; Pred. No. 3e+03;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KVDEQFPQ 12  
 || : ||  
 Db 3 KVGDAIPQ 10

## RESULT 15

A30330  
 neuropeptide pep - California sea hare  
 C:Species: Aplysia californica (California sea hare)  
 C>Date: 02-Feb-1990 #sequence\_revision 02-Feb-1990 #text\_change 09-Jul-2004  
 C:Accession: A30330  
 R:Lloyd, P.E.; Connolly, C.M.  
 J. Neurosci. 9, 312-317, 1989  
 A>Title: Sequence of pedal peptide: a novel neuropeptide from the central nervous system  
 A:Reference number: A30330; MUID:89110403; PMID:2913209  
 A:Accession: A30330  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-15 <LLO>  
 A:Cross-references: UNIPROT:Q7M3P8; UNIPARC:UPI000017BD9A  
 C:Keywords: neuropeptide

Query Match 21.9%; Score 21; DB 2; Length 15;  
 Best Local Similarity 30.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 VDEQFPQHL 15  
 : | : || :  
 Db 2 LDSVYGTHGM 11

Search completed: May 30, 2006, 15:08:20  
 Job time : 13 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2006, 15:01:11 ; Search time 68.6667 Seconds  
(without alignments)  
242,480 Million cell updates/sec

Title: US-10-758-165A-11  
Perfect score: 96  
Sequence: 1 IDGQKXDEQFPQHGLVKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 12648

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 7.2: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	31.2	16	Q7RPP5_PLAYO	Q7RPP5 plasmodium
2	29	30.2	13	Q9UPF7_HUMAN	Q9UPF7 homo sapien
3	28	29.2	14	Q9JUV5_MOUSE	Q9JUV5 mus musculus
4	28	29.2	18	Q8QFT3_CHICK	Q8QFT3 gallus gall
5	25	26.0	14	NSK2_SARBU	NSK2 sarcophaga
6	25	26.0	15	COX5A_SCVCA	COX5A scyllorhinu
7	25	26.0	18	O12692_PPLVG	O12692 simian-huma
8	24	25.0	15	Q7M3W5_APIME	Q7M3W5 apis mellif
9	24	25.0	15	Q9R563_ECOLI	Q9R563 escherichia
10	24	25.0	18	Q4YLT9_PLABE	Q4YLT9 plasmodium
11	24	25.0	18	O5FBR5_SUNMU	O5FBR5 sincus muri
12	24	25.0	18	Q7M198_STRPR	Q7M198 streptomyc
13	23	24.0	11	LSK1_LEBMA	LSK1 leucophaea
14	23	24.0	11	LSKP_PERRAM	LSKP periplaneta
15	23	24.0	14	P78359_HUMAN	P78359 homo sapien
16	23	24.0	15	CX1B_CONBE	CX1B conus betul
17	23	24.0	16	LPHI_CONBE	LPHI conus betul
18	23	24.0	18	O13167_XIPGL	O13167 xiphias gla
19	22	22.9	9	Q7M017_GSTRE	Q7M017 streptococ
20	22	22.9	10	Q5D4Q4_PRHOO	Q5D4Q4 dechloctom
21	22	22.9	11	Q48933_MYCBO	Q48933 mycobacteri
22	22	22.9	11	Q79C20_MYCBO	Q79C20 mycobacteri
23	22	22.9	11	Q79C22_MYCTU	Q79C22 mycobacteri
24	22	22.9	13	Q39380_BRAOL	Q39380 brassica ol
25	22	22.9	13	Q38ZP8_LACSS	Q38ZP8 lactobacill
26	22	22.9	15	ODP3_SOLTU	ODP3 solanum tub
27	22	22.9	16	Q9TRH0_BOVIN	Q9TRH0 bos taurus
28	22	22.9	18	RL24_PROVU	RL24 proteus vul
29	22	22.9	18	Q4XFY5_PLACH	Q4XFY5 plasmodium
30	22	22.9	18	O580F2_GTRYP	O580F2 trypanosoma
31	22	22.9	18	Q9TR15_SHEEP	Q9TR15 ovis aries

32	22	22.9	18	Q8B133_IATK6	Q8B133 influenza a
33	21	21.9	10	CP02_LYCER4	CP02 lycopersico
34	21	21.9	14	GI6S_SPIOL	GI6S spirochaet
35	21	21.9	14	Q9UNN9_HUMAN	Q9UNN9 homo sapien
36	21	21.9	14	Q7M058_MOUSE	Q7M058 mus musculu
37	21	21.9	14	Q65CH4_9GEMI	Q65CH4 tomato leaf
38	21	21.9	15	Q7M3P8_APLGA	Q7M3P8 aplasia cal
39	21	21.9	15	Q61C05_PSEAE	Q61C05 pseudomonas
40	21	21.9	16	Q9UC18_HUMAN	Q9UC18 homo sapien
41	21	21.9	16	Q94F61_WHEAT	Q94F61 triticum ae
42	21	21.9	16	Q44543_ANAVA	Q44543 anabaena va
43	21	21.9	16	Q9R5E9_HAESO	Q9R5E9 haemophilus
44	21	21.9	17	Q3SCF0_9META	Q3SCF0 macropus sp
45	21	21.9	17	Q3SCF2_9META	Q3SCF2 macropus sp

ALIGNMENTS

RESULT 1  
Q7RPP5\_PLAYO PRELIMINARY; PRT; 16 AA.  
ID Q7RPP5\_PLAYO  
AC Q7RPP5;  
DT 15-DEC-2003, integrated into UniProtKB/TREMBL.  
DT 15-DEC-2003, sequence version 1.  
DT 07-FEB-2006, entry version 10.  
DE Hypothetical protein.  
GN ORFNames=PY01411;  
OS Plasmodium yoelli yoelli.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=73239;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=1YXNL;  
RX MEDLINE=22255706; Pubmed=12368865; DOI=10.1038/nature01099;  
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,  
Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,  
Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,  
Shalom S.J., van Aken S.E., Riedmiller S.B., Feldblyum T.V.,  
Cho J.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,  
Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,  
Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,  
van Ijn L.H., Jense C.J., Waters A.P., Smith H.O., White O.R.,  
Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,  
Carucci D.J.;  
"Genome sequence and comparative analysis of the model rodent malaria parasite Plasmodium yoelli yoelli.";  
RL Nature 419:512-519(2002).  
CC -!- CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
preliminary data.  
CC  
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CC  
DR EMBL, ABL01000372; EAA20742.1; -; Genomic\_DNA.  
KW Complete proteome; Hypothetical protein.  
SQ SEQUENCE 16 AA; 1778 MW; 22142D33EC2EE109 CRC64;  
QY Query Match 31.2%; Score 30; DB 2; Length 16;  
Best Local Similarity 62.5%; Pred. No. 1.6e+03;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
Db 1 IDGQKXDE 8  
4 INSKIDE 11  
RESULT 2  
Q9UPF7\_HUMAN PRELIMINARY; PRT; 13 AA.  
ID Q9UPF7\_HUMAN  
AC Q9UPF7;  
DT 01-MAY-2000, integrated into UniProtKB/TREMBL.

```
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Inosine monophosphatase 2 (Fragment).
GN Name=IMP2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN 1
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97463449; PubMed=9322233; DOI=10.1038/sj.mp.4000325;
RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
RA Defera-Wadleigh S.D.;
RT "A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a
RT susceptibility region for bipolar disorder.";
RL Mol. Psychiatry 2:393-397(1997).
[2]
RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=20284187; PubMed=10822344; DOI=10.1038/sj.mp.4000688;
RA Yoshikawa T., Padigaru M., Karkera J.D., Sharma M., Berrettini W.H.,
RA Esterling L.E., Defera-Wadleigh S.D.;
RT "Genomic structure and novel variants of myo-inositol monophosphatase
RT 2.";
RL Mol. Psychiatry 5:165-171(2000).
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DR EMBL; AF025882; AAD22136.1; -; Genomic_DNA.
DR EMBL; AF025881; AAD22136.1; JOINED; Genomic_DNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 13 AA; 1589 MW; F3415D841F48D401 CRC64;

Query Match 30.2%; Score 29; DB 2; Length 13;
Best Local Similarity 36.4%; Pred. No. 1.8e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 8 DEQFPGHGVKQ 18
DB 1 ERFP5HRFIAE 11

RESULT 3
OSJUS MOUSE
ID OSJUS_MOUSE PRELIMINARY; PRT; 14 AA.
AC Q9JUS;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE B-Raf protein (Fragment).
GN Name=B-raf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP NUCLEOTIDE SEQUENCE.
RA Barnier J.V., Papin C., Eychene A., Lecocq O.;
RT "The mouse B-raf gene encodes multiple protein isoforms with tissue-
RT specific expression.";
RL J. Biochem. 270:23381-23389(1995).
[2]
RN NUCLEOTIDE SEQUENCE.
RA Barnier J.V.;
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AJ276308; CAB81556.1; -; mRNA.
```

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DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; RCA.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0003677; F:DNA binding; RCA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; RCA.
DR GO; GO:0008270; F:zinc ion binding; RCA.
DR GO; GO:00050875; P:cellular physiological process; RCA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; RCA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 14 AA; 1748 MW; D1E0505C44927F02 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 DEQFPGHGVKQ 18
DB 1 DEKPEVELDDQ 12

RESULT 4
OSQFT3 CHICK
ID OSQFT3_CHICK PRELIMINARY; PRT; 18 AA.
AC OSQFT3;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Sterol regulatory element binding protein 1 (Fragment).
GN Name=SRBP-1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN 1
RP NUCLEOTIDE SEQUENCE.
RA Asaef S., Pitel F., Morrison M., Alizadeh M., Gondret F., Diot C.,
RA Leclercq B., Vignal A., Douaire M., Lagarrigue S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
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DR EMBL; AJ441122; CAD29619.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 18 AA; 1947 MW; 3206A67750EFD7EA CRC64;

Query Match 29.2%; Score 28; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 7 DEQFPGHGVKQ 18
DB 1 DSPLCNHGKVKQ 12

RESULT 5
NSK2 SARBU
ID NSK2_SARBU STANDARD; PRT; 14 AA.
AC P41493;
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 1.
DT 07-MAR-2006, entry version 32.
DE Neosulfakinin-2 (Neosulfakinin-II) (Neb-SK-II).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga; Neobellieria.
OX NCBI_TaxID=7385;
RN 1
RP PROTEIN SEQUENCE.
```



```

RC TISSUE=Head;
RX MEDLINE=93083101; PubMed=1360367;
RA Ponagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
RT "Isolation and primary structure of two sulfakinin-like peptides from
RL the fleshfly, Neobellieria bullata."
CC Comp. Biochem. Physiol. 103C:135-142(1992).
CC -1- FUNCTION: Myotropic peptide.
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC -----
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CC -----
DR PIR: A56632; A56632.
DR InterPro: IPR013152; Gastrin_CCK.
DR InterPro: IPR013259; Sulfakinin.
DR Pfam: PF08257; Sulfakinin; 1.
DR PROSITE: PS00259; GASTRIN; 1.
KM Annotation: Direct protein sequencing; Neuropeptide; Sulfation.
FT PEPTIDE
FT 1
FT MOD_RES 9
FT MOD_RES 14
FT MOD_RES 14
SQ SEQUENCE 14 Aa; 1796 MW; 8B4E06D5B61C62AA CRC64;

Query Match 26.0%; Score 25; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 9.2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 DEOPFGH 14
Db 3 EEPFDYD 10

RESULT 6
COX5A_SCYCA STANDARD; PRT; 15 Aa.
ID COX5A_SCYCA STANDARD; PRT; 15 Aa.
AC P83012;
DT 29-MAR-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2001, sequence version 1.
DE 07-FEB-2006, entry version 15.
DE Cytochrome c oxidase polypeptide Va, mitochondrial (EC 1.9.3.1)
DE (Fragment).
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Carcharhiniformes;
OC Scyliorhinidae; Scyliorhinus.
OC NCBI_TaxID=7830;
OX NCBI_TaxID=7830;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Rectal gland;
RX MEDLINE=2153426; PubMed=11676495; DOI=10.1006/dbrc.2001.5826;
RA Schuurmans Stekhoven F.M.A.H., Plik G., Wendelaar Bonga S.E.;
RT "N-terminal sequences of small ion channels in rectal glands of
RT sharks: a biochemical hallmark for classification and phylogeny?";
RL Biochem. Biophys. Res. Commun. 288:670-675(2001).
CC -1- FUNCTION: This is the heme A-containing chain of cytochrome c
CC oxidase, the terminal oxidase in mitochondrial electron transport.
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrion, mitochondrial inner membrane.
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase Va family.
CC -----
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CC -----
DR GO: 0005739; C:mitochondrion; IDA.
DR InterPro: IPR003204; Cyt_c-ox5a.
DR Pfam: PF02284; COX5A; 1.
KM Direct protein sequencing; Heme; Inner membrane; Iron; Membrane;
KM Metal-binding; Mitochondrion; Oxidoreductase.
FT CHAIN 1
FT >15 Cytochrome c oxidase polypeptide Va.
FT /FTID=PRO_0000195215.

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FT NON TER 15
SQ SEQUENCE 15 Aa; 1720 MW; 937518D750B35C5 CRC64;

Query Match 26.0%; Score 25; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 9.8e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QKDEQF 10
Db 5 QETDEEF 11

RESULT 7
O12692_9PLVG PRELIMINARY; PRT; 18 Aa.
ID O12692_9PLVG PRELIMINARY; PRT; 18 Aa.
AC O12692;
DT 01-JUL-1997, integrated into UniProtKB/TrEMBL.
DT 01-JUL-1997, sequence version 1.
DT 07-MAR-2006, entry version 26.
DE Gag polyprotein (Fragment).
DE Name=gag;
OS Simian-Human immunodeficiency virus.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentiviruses; Primate lentivirus group.
OC NCBI_TaxID=57667;
OX NCBI_TaxID=57667;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SHIVku1;
RX MEDLINE=97312452; PubMed=9168893; DOI=10.1006/viro.1997.8534;
RA Stephens E.B., Mukherjee S., Sahni M., Zhuge W., Raghavan R.,
RA Singh D.K., Leung K.K., Atkinson R.B., Li Z., Joag S.V., Liu Z.Q.,
RA Narayan O.;
RT "A cell-free stock of simian-human immunodeficiency virus that causes
RT AIDS in pig-tailed macaques has a limited number of amino acid
RT substitutions in both SIVmac and HIV-1 regions of the genome and has
RT offered cytotropism."
RL Virology 231:313-321(1997).
CC -----
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CC -----
DR EMBL: U89249; AAC57878.1; -; Genomic DNA.
DR GO: 0019013; C:Viral nucleocapsid; IEA.
DR GO: 0005198; F:Structural molecule activity; IEA.
DR InterPro: IPR000071; Imm_lenv_matrix.
DR Pfam: PF00540; Gag_p17; 1.
DR Polyprotein.
KM Non TER
FT NON TER 18
FT SEQUENCE 18 Aa; 1961 MW; E064725D22E62EB CRC64;

Query Match 26.0%; Score 25; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 IDGQKVD 8
Db 8 LSGKAD 15

RESULT 8
O7M3M5_APIME PRELIMINARY; PRT; 15 Aa.
ID O7M3M5_APIME PRELIMINARY; PRT; 15 Aa.
AC O7M3M5;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Alpha-glucosidase (EC 3.2.1.20) (Fragment).
OS Apis mellifera (Honeybee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Apidae; Apis.
OX NCBI_TaxID=7460;
RN [1]

```

```

RP PROTEIN SEQUENCE.
RX MEDLINE=97399878; PubMed=9255970;
RA Kimura A., Takara M., Fukushi Y., Mori H., Matsui H., Chiba S.;
RT "A catalytic amino acid and primary structure of active site in
RL Abscixlins niger alpha-glucosidase."
CC Biosci. Biotechnol. Biochem. 61:1091-1098(1997).
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-----
CC
CC PIR; PT0090; PT0090.
DR GO; GO:0004558; F:alpha-glucosidase activity; IEA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 15 AA; 1686 MW; 85730BA8387CB741 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.4e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 IDGOKVD 7
Db 2 IDGFRID 8

RESULT 9
Q9RS63_ECOLI PRELIMINARY; PRT; 15 AA.
AC Q9RS63;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE 40 kDa porin homolog (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=562;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93328296; PubMed=8392972;
RA Dyrco M., Sori R., Cockerill F.III, De Azavedo J., Louie M.,
RT "Multiple determinants of verotoxin-producing Escherichia coli O157:H7
RT attachment-effacement."
RL Infect. Immun. 61:3382-3391(1993).
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-----
CC
CC SEQUENCE 15 AA; 1699 MW; 2767AC9298F8754D CRC64;

Query Match 25.0%; Score 24; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.4e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGOKVD 7
Db 7 DGNKLD 12

RESULT 10
Q4YL79_PLABE PRELIMINARY; PRT; 18 AA.
AC Q4YL79;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein (Fragment).
GN ORFNames=PB400723.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC NCBI_TaxID=5821;
RN [1]

```

```

RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall M., Karras M., Raine J.D., Carlton J.M., Koof J.T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christopoulos G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
-----
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-----
CC
CC EMBL; CAI01003787; CAI01022.1; -; Genomic_DNA.
DR EMBL; CAI01003787; CAI01022.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 18 AA; 2206 MW; EBBABA563A3085A7 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 18;
Best Local Similarity 30.0%; Pred. No. 1.7e+04;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 9 QPQGLVKQ 18
Db 1 KFPKXMMHQ 10

RESULT 11
Q5FBR5_SUNMU PRELIMINARY; PRT; 18 AA.
AC Q5FBR5;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Thiorodoxin (Fragment).
GN Name=TXN;
OS Suncus murinus (House shrew) (Musk shrew).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Insectivora; Soricidae;
OC Crociidae; Suncus.
OC NCBI_TaxID=9378;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=TKU, WZ, and BAN; TISSUE=Kidney;
RX PubMed=15897627; DOI=10.1538/expan.54.173;
RA Adiel S., Sato A., Tanaka S., Kobayashi E., Tanaka K., Nankawa T.,
RA Ishikawa A.;
RT "Development and characterization of CATs markers for genetic linkage
RT mapping in the house musk shrew, Suncus murinus."
RL Exp. Anim. 54:173-180(2005).
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-----
CC
CC EMBL; AB167758; BAD89500.1; -; Genomic_DNA.
DR EMBL; AB167757; BAD89499.1; -; Genomic_DNA.
DR EMBL; AB167756; BAD93380.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 18 AA; 2020 MW; D0B5FC66463A90F8 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.7e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GQKYDE 8
Db 3 GQKYDE 8

```

Db 8 GCKVGE 13

RESULT 12

Q7M198 STRFR PRELIMINARY; PRT; 18 AA.

AC 07M198; Integrated into UniProtKB/TrEMBL.

DT 15-DEC-2003, sequence version 1.

DT 07-FEB-2006, entry version 7.

DE 24k serine proteinase (EC 3.4.21.-) (Fragment).

OS Streptomyces sp.

OC Bacteria; Actinobacteria; Actinomycetales; Streptomyces; Streptomyces; Streptomyces.

NCBI\_TaxID=1906;

OX NCBI\_TaxID=1906;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=9215439; PubMed=1786859; DOI=10.1016/0020-711X(91)90133-8; Slnha U., Wolz S.A., Lad P.J., "Two new extracellular serine proteases from Streptomyces fradiae.", Int. J. Biochem. 23:979-984 (1991).

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CC PIR; A61577; A61577.

FT NON\_TER 1

FT NON\_TER 18

SQ SEQUENCE 18 AA; 2004 MW; 6D6DA167845934A5 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 18;

Best Local Similarity 27.3%; Pred. No. 1.7e+04;

Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 IDGQKVDQFP 11

Db 2 VGGTRAGDEFP 12

RESULT 13

LSK1 LEUMA STANDARD; PRT; 11 AA.

ID AC P04428; Integrated into UniProtKB/Swiss-Prot.

DT 13-AUG-1987, sequence version 1.

DT 13-AUG-1987, entry version 1.

DE Leucosulfakinin-1 (leucosulfakinin-1) (LSK-1).

OS Leucosphaera maderae (Madeira cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea; Blaberidae; Oxyhalotinae; Leucophaea.

NCBI\_TaxID=6988;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=6631585; PubMed=3749893; Nechman R.J., Holman G.M., Haddon W.F., Ling N.; "Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and cholecystokinin.", Science 234:71-73 (1986).

RT Gastrin and cholecystokinin."

RL Science 234:71-73 (1986).

CC -1- FUNCTION: Changes the frequency and amplitude of contractions of the hindgut. Inhibits muscle contraction of hindgut.

CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

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CC PIR; A01622; GMR0L.

DR InterPro; IPR013152; Gastrin\_CCK.

DR InterPro; IPR013259; Sulfakinin.

DR Pfam; PF08257; Sulfakinin; 1.

DR PROSITE; PS00259; GASTRIN; 1.

KW Amdation; Direct protein sequencing; Hormone; Sulfation.

FT PEPTIDE 1

Db 11 Leucosulfakinin-1.

FT MOD\_RES 6 6 /FTID=PRO\_0000043891.

FT MOD\_RES 11 11 Sulfotyrosine.

SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 24.0%; Score 23; DB 1; Length 11;

Best Local Similarity 57.1%; Pred. No. 1.5e+04;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 EQFPQNG 14

Db 1 EQFDYDG 7

RESULT 14

LSKP PERAM STANDARD; PRT; 11 AA.

ID AC P36885; Integrated into UniProtKB/Swiss-Prot.

DT 01-JUN-1994, sequence version 1.

DT 01-JUN-1994, entry version 29.

DE Perisulfakinin (Pea-SK-I).

OS Periplaneta americana (American cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattelloidea; Blattidae; Blattinae; Periplaneta.

NCBI\_TaxID=6978;

OX NCBI\_TaxID=6978;

RN [1]

RP PROTEIN SEQUENCE.

RX TISSUE=Corpora cardiaca; MEDLINE=90137190; PubMed=2615921; DOI=10.1016/0143-4179(89)90038-3; Venestra J.A.; "Isolation and structure of two gastrin/CCK-like neuropeptides from the American cockroach homologous to the leucosulfakinins.", Neuropeptides 14:145-149 (1989).

RT the American cockroach homologous to the leucosulfakinins."

RL Neuropeptides 14:145-149 (1989).

CC -1- FUNCTION: Stimulates hindgut contractions.

CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

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CC PIR; A06566; A06566.

DR InterPro; IPR013152; Gastrin\_CCK.

DR InterPro; IPR013259; Sulfakinin.

DR Pfam; PF08257; Sulfakinin; 1.

DR PROSITE; PS00259; GASTRIN; 1.

KW Amdation; Direct protein sequencing; Hormone; Sulfation.

FT PEPTIDE 1

FT MOD\_RES 6 6 /FTID=PRO\_0000043893.

FT MOD\_RES 11 11 Sulfotyrosine.

SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAB CRC64;

Query Match 24.0%; Score 23; DB 1; Length 11;

Best Local Similarity 57.1%; Pred. No. 1.5e+04;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 EQFPQNG 14

Db 1 EQFDYDG 7

RESULT 15

P78359 HUMAN PRELIMINARY; PRT; 14 AA.

ID AC P78359; Integrated into UniProtKB/TrEMBL.

DT 01-MAY-1997, sequence version 1.

DT 01-MAY-1997, entry version 17.

DE NF-kappa-B transcription factor p65 (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

```
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Umbilical vein;
RA Remacle J.E., Brys R., Pype S., Nelles L., Huybrecock D.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; U88316; AAB48487.1; -; mRNA.
FT NON TER 14
SQ SEQUENCE 14 AA; 1662 MW; 5E30458F8262F957 CRC64;

Query Match 24.0%; Score 23; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 2e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 VDEQFP 11
   :|||
Db 1 MDELFP 6
```

Search completed: May 30, 2006, 15:07:38  
Job time : 70.6667 secs

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 30, 2006, 14:59:31 ; Search time 61.6667 Seconds  
(without alignments)  
133.458 Million cell updates/sec

Title: US-10-758-165A-11  
Perfect score: 96  
Sequence: 1 IDGQKVDQFPQHGVLKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 902922

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*
- 9: geneseqp2005s:\*
- 10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	96	100.0	18	ADRI0611
2	78	81.2	15	ADG64569
3	36	37.5	14	ABP46438
4	36	37.5	14	ADG97265
5	36	37.5	14	AED79318
6	35	36.5	16	AEE33637
7	35	36.5	16	AEE34193
8	35	36.5	18	ADRI0610
9	34	35.4	15	AAK50232
10	34	35.4	15	ABP94693
11	34	35.4	15	ABP95588
12	34	35.4	15	ABP95194
13	34	35.4	17	ADM96833
14	34	35.4	18	ADRI0609
15	33	34.4	10	ADL98126
16	33	34.4	13	ADG95486
17	33	34.4	15	ABP94247
18	33	34.4	15	ABP95584
19	33	34.4	15	ABP94098
20	33	34.4	15	ABP95117
21	33	34.4	15	ABP94539
22	33	34.4	15	ABP94780
23	33	34.4	15	ABP95372

24	33	34.4	15	ABR32079	ABP32079 Human can
25	33	34.4	15	ABR32127	ABP32127 Human can
26	33	34.4	15	ADV31901	ADV31901 Human 109
27	33	34.4	15	ADV31853	ADV31853 Human 109
28	33	34.4	15	AEC70956	AEC70956 Human 109
29	33	34.4	15	AEC70908	AEC70908 Human 109
30	33	34.4	15	AEE34208	AEE34208 Wheat g11
31	33	34.4	15	AEE33641	AEE33641 Wheat g11
32	32	33.3	10	AAW15125	AAW15125 Aspergill
33	32	33.3	14	AAQ98200	AAQ98200 Human SNP
34	32	33.3	14	ABP46692	ABP46692 Human Bly
35	32	33.3	14	ABP46435	ABP46435 Human Bly
36	32	33.3	14	ADG97262	ADG97262 scfV VHCD
37	32	33.3	14	ADG97519	ADG97519 scfV VHCD
38	32	33.3	14	AED79315	AED79315 Human B L
39	32	33.3	14	AED79572	AED79572 Human B L
40	32	33.3	15	ABP95187	ABP95187 HLA prote
41	32	33.3	15	ABP94687	ABP94687 HLA prote
42	32	33.3	15	ABP94184	ABP94184 HLA prote
43	32	33.3	15	ABP94689	ABP94689 HLA prote
44	32	33.3	15	ABP95591	ABP95591 HLA prote
45	32	33.3	15	ABP95184	ABP95184 HLA prote

## ALIGNMENTS

RESULT 1  
ID ADR10611 standard; peptide: 18 AA.  
XX ADR10611;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
XX Horse IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 11.  
DE  
XX Antiacetaminic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
KW horse.  
XX  
XX Equus caballus.  
XX  
PD WO2004065936-A2.  
XX  
XX 05-AUG-2004.  
XX  
XX 15-JAN-2004; 2004WO-US003566.  
XX  
XX 16-JAN-2003; 2003US-0440472P.  
XX  
XX (UYNC-) UNIV NORTH CAROLINA STATE.  
XX  
XX Hammerberg B;  
XX  
XX WPI; 2004-593545/57.  
XX  
XX Novel antibody that specifically binds to mammalian IGE epitope, useful  
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
PT or treating asthma or anaphylactic shock.  
XX  
XX Example 6; Page 9; 14pp; English.  
XX  
XX The present invention relates to a novel monoclonal antibody (1) that  
CC specifically binds to a mammalian IGE epitope, where the epitope is  
CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
CC (1) is useful for testing an allergen reactivity of an IGE sample. The  
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
CC and corn allergens. The sample is a biological sample collected from a  
CC dog, cat or horse. (1) is also useful for detecting mammalian IGE and for  
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
CC antibodies recognise epitopes on canine IGF corresponding to amino acid  
CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the

CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC horse IGE 3.76 recognition site.  
 CC  
 XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 96; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHGVLVKQ 18  
 |||||  
 1 IDGQKVDQFPQHGVLVKQ 18

Db 1 IDGQKVDQFPQHGVLVKQ 18

RESULT 2

ADG64569  
 ID ADG64569 standard; peptide; 15 AA.

AC ADG64569;

DT 18-DEC-2003 (first entry)

DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide p5.

XX Horse; immunoglobulin E; IGE; heavy chain; immunogen; allergy.

OS Equus caballus.

XX US2003087314-A1.

PN 08-MAY-2003.

XX 08-NOV-2001; 2001US-00052788.

XX 08-NOV-2001; 2001US-00052788.

PA (REGC ) UNIV CALIFORNIA.

PI Gershwin LJ, Pettigrew HD, Kalina WJ;

DR WPI; 2003-765437/72.

PT Immunogenic composition comprising an isolated equine immunoglobulin E  
 PT polypeptide that induces production of antibodies which specifically bind  
 PT to equine immunoglobulin E.  
 XX

XX Example 1; Page 8; 14pp; English.

XX The invention relates to an immunogenic composition comprising an  
 CC isolated polypeptide having an amino acid sequence that is at least 80%  
 CC identical to 6 (SI-56), 15 amino acid peptide sequences derived from  
 CC equine immunoglobulin E (the composition induces production of an  
 CC antibody that specifically binds to equine immunoglobulin (Ig)E), the six  
 CC polypeptides are not explicitly identified in the specification. Also  
 CC included are a composition comprising an antibody that specifically binds  
 CC to a polypeptide at least 80% identical to (SI)-(56), an antibody that  
 CC specifically binds to equine IGE made by the process of immunising an  
 CC animal with a polypeptide at least 80% identical to (SI)-(56), making an  
 CC antibody that specifically binds to equine IGE (involving immunising an  
 CC animal with a composition further comprising an isolated polypeptide (the  
 CC amino acid sequence of the polypeptide is at least 80% identical to (SI)-  
 CC (56)), and collecting antiserum from the animal) and a kit for detection  
 CC of equine IGE in a biological sample comprising the antibody and means  
 CC for detecting specific binding of the antibody to equine IGE. The  
 CC antibody is useful for detecting equine IGE protein in a biological  
 CC sample (serum) which involves contacting the sample with the antibody,  
 CC thus forming an antigen/antibody complex, and detecting the presence or  
 CC absence of the antigen/antibody complex. The antibody and antigen are  
 CC immobilised on a solid surface. The antibody is labelled such that the

CC complex can be detected. The complex is detected using a second labelled  
 CC antibody. The peptides are useful for generating antibodies specific for  
 CC IGE which can serve as a diagnostic test for allergy. The present  
 CC sequence is a horse immunoglobulin E, IGE, heavy chain immunogenic  
 CC peptide from the middle portion of the C2 region.  
 CC  
 XX

SQ Sequence 15 AA;

Query Match 81.2%; Score 78; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHG 14  
 |||||  
 2 IDGQKVDQFPQHG 15

Db 2 IDGQKVDQFPQHG 15

RESULT 3

ABP46438  
 ID ABP46438 standard; peptide; 14 AA.

AC ABP46438;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv VH CDR3 SEQ ID 2449.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;  
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;  
 KW immunosuppressive; immunostimulant; immunomodulatory; antineutritic;  
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;  
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;  
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

OS WO200202641-A1.

XX 10-JAN-2002.

XX 15-JUN-2001; 2001WO-US019110.

XX 16-JUN-2000; 2000US-0212210P.

XX 17-OCT-2000; 2000US-0240816P.

XX 16-MAR-2001; 2001US-0276248P.

XX 21-MAR-2001; 2001US-0277379P.

XX 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

DR WPI; 2002-114799/15.

PT Antibodies against B lymphocyte stimulating polypeptides, useful for the  
 PT diagnosis and treatment of cancers and immune disorders.  
 XX

XX Claim 2; Page 2992; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to  
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the  
 CC tumour necrosis factor (TNF) super family and induces B cell  
 CC proliferation and differentiation. The antibodies of the invention have  
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,  
 CC antineutritic and antiAIDS activity and can be used in vaccines to  
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys  
 CC and so may be used to detect and quantitate the presence of Blys in  
 CC biological samples and may be used in this way to diagnose disease  
 CC associated with aberrant expression of Blys. They may also be  
 CC administered to treat diseases associated with aberrant Blys expression  
 CC and activity such as cancer, immune, and autoimmune disorders and  
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,

CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and  
CC acquired immunodeficiency syndrome (AIDS)). ABB43990-ABB47228 represent  
CC the antibodies and fragments of the antibodies described in the method of  
CC the invention  
XX

XX Sequence 14 AA:

Query Match 37.5%; Score 36; DB 5; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 FPOHGL 15  
| | | | |  
Db 7 FPOHGL 12

RESULT 4  
ADG97265  
ID ADG97265 standard; peptide: 14 AA.

XX ADG97265;

DT 11-MAR-2004 (first entry)

DE scFv VHCDR3 peptide that immunospecifically binds BlyS SeqID 2449.

XX antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;  
KM B cell proliferation; differentiation; scFv; myasthenia gravis;  
KM multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;  
KM carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;  
KM antiinflammatory; antiallergic; antiallergic; cytostatic.

XX Unidentified.

XX W02003055979-A2.

XX 10-JUL-2003.

XX 14-NOV-2002; 2002MO-US036496.

XX 16-NOV-2001; 2001US-0331469P.  
PR 19-DEC-2001; 2001US-0340817P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;  
PI WPI; 2003-505530/47.

PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator  
PT (BlyS), useful for detecting and treating diseases or disorders e.g.  
PT rheumatoid arthritis, asthma and leukemia.

XX Example 1; SEQ ID NO 2449; 394pp; English.

XX This invention relates to novel antibodies that immunospecifically bind  
CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to  
CC chromosome 13q34 and encodes a protein that is a member of the tumour  
CC necrosis factor superfamily and induces both in vivo and in vitro B cell  
CC proliferation and differentiation. Specifically, it refers to single  
CC chain antibody molecules (scFvs) derived, preferably, from the variable  
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or  
CC fragment thereof, of either human, murine, rat or monkey BlyS. The  
CC present invention refers to the use of such antibodies in various methods  
CC for the detection, diagnosis and prognosis of diseases related to the  
CC aberrant expression or inappropriate function of BlyS or its receptor. As  
CC such, these compositions are useful for identifying immune disorders  
CC including myasthenia gravis and multiple sclerosis, inflammatory  
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such  
CC as AIDS and proliferative disorders including leukaemia, carcinoma and  
CC lymphoma. Accordingly, they can be described as exhibiting various  
CC activities such as antirheumatic, antiallergic, neuroprotective,  
CC antiinflammatory, antiallergic, antiallergic and cytostatic. This

CC peptide sequence is a single chain antibody variable heavy CDR3 peptide  
CC that immunospecifically binds BlyS of the invention.

XX Sequence 14 AA:

Query Match 37.5%; Score 36; DB 7; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 FPOHGL 15  
| | | | |  
Db 7 FPOHGL 12

RESULT 5  
AED79318  
ID AED79318 standard; peptide: 14 AA.

XX AED79318;

DT 12-JAN-2006 (first entry)

DE Human B lymphocyte binding scFv VH CDR3 peptide, SEQ ID 2449.

XX Antiinflammatory; Dermatological; Immunosuppressive; Antirheumatic;  
KM Antiarthritic; Neuroprotective; Muscular-Gen.; Antiallergic;  
KM Antiallergic; Anticarcinogenic; Anti-HIV; Cytostatic; B-lymphocyte;  
KM antibody; autoimmune disease; B-cell lymphoma;  
KM systemic lupus erythematosus; rheumatoid arthritis; immune disorder;  
KM inflammation; infectious disease; hyperproliferation.

XX Homo sapiens.

XX US200525532-A1.

XX 17-NOV-2005.

XX 10-FEB-2005; 2005US-00054515.

XX 16-JUN-2000; 2000US-0212210P.  
PR 17-OCT-2000; 2000US-0240816P.  
PR 16-MAR-2001; 2001US-0276248P.  
PR 21-MAR-2001; 2001US-0277379P.  
PR 25-MAY-2001; 2001US-0293499P.  
PR 15-JUN-2001; 2001US-00880748.  
PR 16-NOV-2001; 2001US-0331469P.  
PR 19-DEC-2001; 2001US-0340817P.  
PR 14-NOV-2002; 2002US-00293418.  
PR 11-FEB-2004; 2004US-0543296P.  
PR 18-JUN-2004; 2004US-0380347P.

XX (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
PA (CHOI/) CHOI G H.  
PA (VAUG/) VAUGHAN T.  
PA (HILB/) HILBERT D.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;  
PI WPI; 2005-808635/82.

PT New antibodies that immunospecifically binds to B lymphocyte stimulator  
PT protein, useful for diagnosing, treating, or preventing autoimmune  
PT disease, e.g. systemic lupus erythematosus or rheumatoid arthritis, or B  
PT cell cancer.

XX Example 1; SEQ ID NO 2449; 240pp; English.

XX The invention relates to a novel antibody that immunospecifically binds  
CC to B lymphocyte stimulator protein. The protein comprises an amino acid  
CC sequence that is 85% identical to the VH domain of any one of the single-  
CC chain variable fragments (scFvs) of SEQ ID NOs. 1-2128, and/or an amino  
CC acid sequence that is at least 85% identical to the VL domain of any one

CC of the seqs of SEQ ID NOs. 1-2128. The invention further comprises: an  
CC isolated nucleic acid molecule encoding the antibody; an isolated cell  
CC line that expresses the antibody; a method for detecting the expression  
CC of a B lymphocyte Stimulator protein; a method for diagnosing an  
CC autoimmune disease or a B cell cancer; and a method for treating,  
CC preventing, or ameliorating an autoimmune disease or a B cell cancer. The  
CC antibody is useful for detecting expression of B lymphocyte Stimulator  
CC protein, and in diagnosing, treating, preventing, or ameliorating an  
CC autoimmune disease or a B cell cancer. The autoimmune disease is systemic  
CC lupus erythematosus or rheumatoid arthritis. It can also be used for  
CC diagnosing, treating, and preventing immune disorders (e.g. multiple  
CC sclerosis, myasthenia gravis, or Hashimoto's disease), inflammatory  
CC disorders (e.g. asthma or allergic disorders), infectious diseases (e.g.  
CC AIDS), and proliferative disorders (e.g. leukemia, carcinoma, or  
CC lymphoma). This sequence represents the heavy chain variable  
CC complementary determining region 3 of a single-chain variable fragment  
CC polypeptide that immunospecifically binds to a B lymphocyte Stimulator  
CC protein of the invention. Note: This sequence is not shown in the  
CC specification. It has been electronically downloaded from the USPTO  
CC website.

CC XX Sequence 14 AA;

Query Match 37.5%; Score 36; DB 9; Length 14;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 10 FPOHGL 15  
|||  
7 FPOHGL 12

Db

RESULT 6

ID AEE33637 standard; peptide; 16 AA.

AC AEE33637;

DT 09-FEB-2006 (first entry)

DE Wheat gliadin/glutelin epitope SEQ ID NO 323.

XX Immunosuppressive; Gastrointestinal-Gen.; T-cell-receptor-agonist;  
KM T-cell-receptor-antagonist; Vaccine; celiac disease; immunogenicity;  
KM gastrointestinal disease; immune disorder; gluten protein; gliadin.

XX Triticum aestivum.

XX WO2005105129-A2.

XX 10-NOV-2005.

XX 28-APR-2005; 2005WO-GB001621.

XX 28-APR-2004; 2004AU-00201774.

PR 11-FEB-2005; 2005AU-00900650.

XX (BTGT-) BTG INT LTD.

PI Anderson R, Beisbach T, Din JT;

DR WPI; 2005-769484/78.

PT Preventing or treating celiac disease comprises administering to an  
PT individual a peptide (analogue) comprising at least one T cell epitope  
PT (e.g. a wheat and/or an oat epitope).

PS Claim 1; SEQ ID NO 323; 94pp; English.

CC The invention relates to a method of preventing or treating celiac  
CC disease comprises administering to an individual at least one agent  
CC selected from a peptide comprising at least one epitope, given in the  
CC specification, or their equivalents, and an analogue of the peptide,

CC which is capable of being recognized by a T cell receptor that recognizes  
CC the peptide. The methods, agents, antagonists and compositions are useful  
CC for treating or preventing celiac disease. The agent or antagonist, or  
CC wild type sequence is useful for producing an antibody specific to the  
CC agent, antagonist or wild type sequence. The mutation in an epitope of a  
CC gluten protein is useful for decreasing the ability of the gluten protein  
CC to cause celiac disease. The present sequence represents the amino acid  
CC sequence of a wheat gliadin/glutelin epitope.

CC XX Sequence 16 AA;

Query Match 36.5%; Score 35; DB 9; Length 16;  
Best Local Similarity 54.5%; Pred. No. 1.8e+02;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 4 QKVDQFPQHG 14  
: : : : :  
6 QQPEQDFPQFG 16

Db

RESULT 7

ID AEE34193 standard; peptide; 16 AA.

AC AEE34193;

DT 09-FEB-2006 (first entry)

DE Wheat gliadin/glutelin epitope SEQ ID NO 879.

XX Immunosuppressive; Gastrointestinal-Gen.; T-cell-receptor-agonist;  
KM T-cell-receptor-antagonist; Vaccine; celiac disease; immunogenicity;  
KM gastrointestinal disease; immune disorder; gluten protein; gliadin.

XX Triticum aestivum.

XX WO2005105129-A2.

XX 10-NOV-2005.

XX 28-APR-2005; 2005WO-GB001621.

XX 28-APR-2004; 2004AU-00201774.

PR 11-FEB-2005; 2005AU-00900650.

XX (BTGT-) BTG INT LTD.

PI Anderson R, Beisbach T, Din JT;

DR WPI; 2005-769484/78.

PT Preventing or treating celiac disease comprises administering to an  
PT individual a peptide (analogue) comprising at least one T cell epitope  
PT (e.g. a wheat and/or an oat epitope).

PS Claim 1; SEQ ID NO 879; 94pp; English.

CC The invention relates to a method of preventing or treating celiac  
CC disease comprises administering to an individual at least one agent  
CC selected from a peptide comprising at least one epitope, given in the  
CC specification, or their equivalents, and an analogue of the peptide,  
CC which is capable of being recognized by a T cell receptor that recognizes  
CC the peptide. The methods, agents, antagonists and compositions are useful  
CC for treating or preventing celiac disease. The agent or antagonist, or  
CC wild type sequence is useful for producing an antibody specific to the  
CC agent, antagonist or wild type sequence. The mutation in an epitope of a  
CC gluten protein is useful for decreasing the ability of the gluten protein  
CC to cause celiac disease. The present sequence represents the amino acid  
CC sequence of a wheat gliadin/glutelin epitope.

CC XX Sequence 16 AA;

SQ

Query Match 36.5%; Score 35; DB 9; Length 16;





```

PD    24-OCT-2002.
PF    09-APR-2002; 2002WO-USO11359.
XX
XX    10-APR-2001; 2001US-0282739P.
PR    25-APR-2001; 2001US-0286630P.
PR    22-JUN-2001; 2001US-0300373P.
XX
PA    (AGEN-) AGENSYS INC.
PI    Chailita-Bid PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;
PI    Afar DBH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits AJ;
XX
DR    WPI; 2003-092956/08.
XX
PT    New composition comprising a substance that modulates the status of
PT    12IP2A polypeptides, useful for eliciting humoral or cellular immune
PR    responses or in assessing the status of 12IP2A3 gene products in normal
XX    versus cancerous tissues.
XX
PS    Claim 13; Page 287; 362pp; English.
XX
CC    The invention relates to a novel composition comprising a substance that
CC    modulates the status of a protein, 12IP2A3. The composition of the
CC    invention has cytosstatic and immunostimulant activity, and is useful as a
CC    vaccine. The 12IP2A3 proteins and polynucleotides are useful for
CC    eliciting humoral or cellular immune response. The polynucleotides are
CC    useful for characterising cytogenetic abnormalities of this chromosomal
CC    locus, as tools that can be used to delineate cytogenetic abnormalities
CC    in the chromosomal region that encodes 12IP2A3 that may contribute to
CC    malignant phenotype, and in assessing the status of 12IP2A3 gene products
CC    in normal versus cancerous tissues. The proteins are useful for
CC    generating and characterising domain-specific antibodies, for identifying
CC    agents or cellular factors that bind to 12IP2A3 or a particular structure
CC    domain, and in various therapeutic and diagnostic contexts, including
CC    cancer vaccines. The antibodies or T cells reactive with the product are
CC    useful in passive or active immunisation, and in imaging methodologies
CC    for the management of cancer. The sequences shown in ABP83646 - ABP95595
XX    represent peptides from the 12IP2A3 variants of the invention
SQ
SQ    Sequence 15 AA;
Query Match      35.4%; Score 34; DB 6; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY          2 DGKVKDEQFPOGLV 16
           :|:||||:
Db          1 ENKKDKROHVQHLL 15
RESULT 12
ABP95194
ID   ABP95194 standard; peptide; 15 AA.
XX
AC   ABP95194;
XX
DT   28-MAR-2003 (first entry)
XX
DE   HLA protein 12IP2A3 peptide #11549.
XX
KW   Human; 12IP2A3; cytosstatic; immunostimulant; vaccine; SSH;
KW   humoral immune response; cellular immune response;
KW   suppresion substrate hybridisation; HLA; human leukocyte antigen.
XX
OS   Homo sapiens.
XX
PN   WO200283068-A2.
XX
PD   24-OCT-2002.
PF   09-APR-2002; 2002WO-USO11359.
XX

```

PR 10-APR-2001; 2001US-0282739P.  
PR 25-APR-2001; 2001US-0286630P.  
PR 22-JUN-2001; 2001US-0300373P.  
XX  
XX (AGEN-) AGENSYS INC.  
XX  
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;  
PI Alar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;  
XX WPI; 2003-092956/08.  
XX  
XX  
PT New composition comprising a substance that modulates the status of  
PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune  
PT responses or in assessing the status of 121P2A3 gene products in normal  
PT versus cancerous tissues.  
XX  
XX Claim 13; Page 279; 362pp; English.  
XX  
CC The invention relates to a novel composition comprising a substance that  
CC modulates the status of a protein, 121P2A3. The composition of the  
CC invention has cytosolic and immunostimulant activity, and is useful as a  
CC vaccine. The 121P2A3 proteins and polynucleotides are useful for  
CC eliciting humoral or cellular immune response. The polynucleotides are  
CC useful for characterizing cytogenetic abnormalities of this chromosomal  
CC locus, as tools that can be used to delineate cytogenetic abnormalities  
CC in the chromosomal region that encodes 121P2A3 that may contribute to  
CC malignant phenotype, and in assessing the status of 121P2A3 gene products  
CC in normal versus cancerous tissues. The proteins are useful for  
CC generating and characterizing domain-specific antibodies, for identifying  
CC agents or cellular factors that bind to 121P2A3 or a particular structure  
CC domain, and in various therapeutic and diagnostic contexts, including  
CC cancer vaccines. The antibodies or T cells reactive with the product are  
CC useful in passive or active immunisation, and in imaging methodologies  
CC for the management of cancer. The sequences shown in ABP83646 - ABP95595  
CC represent peptides from the 121P2A3 variants of the invention  
XX  
SQ Sequence 15 AA;  
SQ  
Query Match 35.4%; Score 34; DB 6; Length 15;  
Best Local Similarity 40.0%; Pred. No. 2.4e+02;  
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;  
Qy 2 DGQKVDQFPQHGIV 16  
Db 1 ENKLDROHVQHLL 15  
RESULT 13  
ADM96833  
ID ADM96833 standard; peptide; 17 AA.  
XX  
XX ADM96833;  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Tissue factor VIIA (TFVIIa) peptide antagonist #249.  
XX  
XX Tissue Factor VIIa; TFVIIa; chronic thromboembolic disease;  
XX fibrin formation; vascular disorders; deep venous thrombosis;  
XX arterial thrombosis; stroke; atherosclerosis; septicemia.  
XX  
XX Synthetic.  
XX  
XX US2004087767-A1.  
XX  
XX 06-MAY-2004.  
XX  
XX 30-JAN-2003; 2003US-00356257.  
XX  
XX 06-FEB-2002; 2002US-0355420P.  
XX  
XX (GETH ) GENENTECH INC.  
XX

PI Lazarus RA, Maun HR;  
XX WPI; 2004-356247/33.  
XX  
XX  
XX New peptide, useful for preventing or treating chronic thromboembolic  
XX diseases or disorders associated with fibrin formation including vascular  
XX disorders, such as deep venous thrombosis, arterial thrombosis, and  
XX stroke.  
XX  
XX Example 2; SEQ ID NO 255; 102pp; English.  
XX  
XX  
CC The invention relates to peptide antagonists of tissue Factor VIIa  
CC (TFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa  
CC with the peptide in the presence of tissue factor and under conditions  
CC that allow binding of the compound to FVIIa to occur. The peptides are  
CC useful for preventing or treating chronic thromboembolic diseases or  
CC disorders associated with fibrin formation including vascular disorders,  
CC such as deep venous thrombosis, arterial thrombosis, stroke,  
CC atherosclerosis, or septicemia. The present sequence represents a TFVIIa  
CC peptide antagonist of the invention.  
XX  
XX  
SQ Sequence 17 AA;  
SQ  
Query Match 35.4%; Score 34; DB 8; Length 17;  
Best Local Similarity 50.0%; Pred. No. 2.7e+02;  
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;  
Qy 3 GQKVDQFPQ 12  
Db 1 GEGVEEPPE 10  
RESULT 14  
ADR10609  
ID ADR10609 standard; peptide; 18 AA.  
XX  
XX ADR10609;  
XX  
XX 21-OCT-2004 (first entry)  
XX  
DE Dog IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 9.  
XX  
XX  
XX Antiaerthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
XX anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.  
XX  
XX Canis familiaris.  
XX  
XX WO2004065936-A2.  
XX  
XX 05-AUG-2004.  
XX  
XX 15-JAN-2004; 2004WO-US003566.  
XX  
XX 16-JAN-2003; 2003US-0440472P.  
XX  
XX (UNNC-) UNIV NORTH CAROLINA STATE.  
XX  
XX Hammerberg B;  
XX  
XX WPI; 2004-593545/57.  
XX  
XX  
XX Novel antibody that specifically binds to mammalian IGE epitope, useful  
XX for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
XX or treating asthma or anaphylactic shock.  
XX  
XX Example 6; Page 9; 14pp; English.  
XX  
XX The present invention relates to a novel monoclonal antibody (I) that  
XX specifically binds to a mammalian IGE epitope, where the epitope is  
XX between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
XX (I) is useful for testing an allergen reactivity of an IGE sample.  
XX CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
XX and corn allergens. The sample is a biological sample collected from a

dog, cat or horse. (1) is also useful for detecting mammalian IGE and for  
treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
antibodies recognise epitopes on canine IGE corresponding to amino acid  
residues 357-371 (ADR1601) and 146-162 (ADR1009) respectively of the  
canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
3.76 were observed to have good cross-reactivity with the epsilon-chain  
of IGE from cat and horse, but did not exhibit cross-reactivity with  
either pig or human epsilon-chains of IGE.

Sequence 18 AA;

Query Match 35.4%; Score 34; DB 8; Length 18;

Best Local Similarity 54.5%; Pred. No. 2.9e+02;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 IDGQVDEQFP 11  
:|||||  
1 VDGQKATNIFP 11

Db 1 VDGQKATNIFP 11

RESULT 15

ADL98126 standard; peptide; 10 AA.

ADL98126;

17-JUN-2004 (first entry)

Candida kefyr enone reductase peptide SEQ ID NO:9.

enone reductase; enzyme; levodione; ketoisophorone; carotenoid;

Candida kefyr; Kluyveromyces marxianus.

Kluyveromyces marxianus.

WO2004027065-A2.

01-APR-2004.

19-SEP-2003; 2003WO-EP010473.

23-SEP-2002; 2002EP-00021098.

(STAM ) DSM IP ASSETS BV.

Kataoka M, Shimizu S;

WPI; 2004-295422/27.

New enone reductase, useful in improving the production process of  
levodione, which is important in the synthesis of optically active  
carotenoids.

Example 1; SEQ ID NO 9; 31pp; English.

The present invention describes an isolated DNA (I) comprising a  
nucleotide sequence coding for an enzyme having enone reductase activity.  
Also described: (1) a vector or a plasmid comprising (I); (2) a host cell  
transformed or transfected by (1) or the vector or the plasmid of (1);  
(3) a polypeptide encoded by (1); and (4) a process for the production of  
levodione which comprises contacting ketoisophorone with the polypeptide  
of (3) or with the host cell of (2) or a cell-free extract under  
conditions for the production of levodione, e.g. at pH 4.0-9.0 and at a  
temperature of 10-60 degrees Celsius for 5 minutes to 72 hours or at pH  
5.0-8.0 and at a temperature of 20-60 degrees Celsius for 15 minutes to  
48 hours. The DNA (I) and the encoded polypeptide can be used in  
improving the production process of levodione, which is important in the  
synthesis of optically active carotenoids. The present sequence  
represents a Candida kefyr (Kluyveromyces marxianus) enone reductase  
peptide, which is used in the exemplification of the present invention.

Sequence 10 AA;

Query Match 34.4%; Score 33; DB 8; Length 10;  
Best Local Similarity 71.4%; Pred. No. 2.2e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 11 POGGLVVK 17  
:|||||  
4 POGGITK 10

Db 4 POGGITK 10

Search completed: May 30, 2006, 15:04:05  
Job time : 63.6667 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

## OM protein - protein search, using sw model

Run on: May 30, 2006, 15:17:23 ; Search time 49.3333 Seconds  
(without alignments)  
169.011 Million cell updates/sec

Title: US-10-758-165A-11

Perfect score: 96

Sequence: 1 IDGQKVDQEPFGHGLVQK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 432914

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:\*

1: /EMC\_Celerra\_sids3/ptodata/2/pubppa/us07\_PUBCOMB.pep:\*

2: /EMC\_Celerra\_sids3/ptodata/2/pubppa/us08\_PUBCOMB.pep:\*

3: /EMC\_Celerra\_sids3/ptodata/2/pubppa/us09\_PUBCOMB.pep:\*

4: /EMC\_Celerra\_sids3/ptodata/2/pubppa/us10\_PUBCOMB.pep:\*

5: /EMC\_Celerra\_sids3/ptodata/2/pubppa/us10B\_PUBCOMB.pep:\*

6: /EMC\_Celerra\_sids3/ptodata/2/pubppa/us11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	18	5	US-10-758-165-11
2	78	81.2	15	4	US-10-052-788-5
3	36	37.5	14	3	US-09-880-748-2449
4	36	37.5	14	4	US-10-293-418-2449
5	36	37.5	14	6	US-11-054-515-2449
6	36	37.5	14	6	US-11-266-444-2449
7	35	36.5	15	4	US-10-758-165-10
8	34	35.4	15	4	US-10-141-627-11
9	34	35.4	17	4	US-10-356-257-255
10	34	35.4	17	5	US-10-758-165-9
11	33	34.4	13	6	US-11-127-804-9
12	32	33.3	10	4	US-10-079-709-3
13	32	33.3	10	6	US-11-036-272-3
14	32	33.3	14	3	US-09-880-748-2703
15	32	33.3	14	3	US-09-880-748-2446
16	32	33.3	14	4	US-10-293-418-2446
17	32	33.3	14	4	US-10-293-418-2703
18	32	33.3	14	5	US-10-865-478-842
19	32	33.3	14	6	US-11-054-515-2446
20	32	33.3	14	6	US-11-054-515-2703
21	32	33.3	14	6	US-11-266-444-2446
22	32	33.3	14	6	US-11-266-444-2703
23	31	32.3	14	6	US-09-880-748-2146
24	31	32.3	14	3	US-09-880-748-2151
25	31	32.3	14	4	US-10-293-418-2146
26	31	32.3	14	4	US-10-293-418-2151
27	31	32.3	14	6	US-11-054-515-2146

28	31	32.3	14	6	US-11-054-915-2151	Sequence 2151, Ap
29	31	32.3	14	6	US-11-266-444-2146	Sequence 2146, Ap
30	31	32.3	14	6	US-11-266-444-2151	Sequence 2151, Ap
31	31	32.3	15	4	US-10-059-261-108	Sequence 108, App
32	31	32.3	15	4	US-10-059-261-216	Sequence 216, App
33	31	32.3	15	5	US-10-627-649-108	Sequence 108, App
34	31	32.3	15	5	US-10-627-649-216	Sequence 216, App
35	31	32.3	18	5	US-10-758-165-15	Sequence 15, App1
36	30	31.2	10	4	US-10-353-929-166	Sequence 166, App
37	30	31.2	11	3	US-09-977-827-8	Sequence 8, App11
38	30	31.2	17	3	US-09-864-761-46580	Sequence 46580, A
39	29.5	30.7	17	4	US-10-356-257-114	Sequence 114, App
40	29	30.2	11	3	US-09-977-827-13	Sequence 13, App1
41	29	30.2	12	5	US-10-500-878-14	Sequence 14, App1
42	29	30.2	13	6	US-11-152-974A-272	Sequence 272, App
43	29	30.2	13	6	US-11-153-143A-272	Sequence 272, App
44	29	30.2	14	5	US-10-476-362-26	Sequence 26, App1
45	29	30.2	15	4	US-10-282-960-23	Sequence 23, App1

## ALIGNMENTS

```
RESULT 1
US-10-758-165-11
; Sequence 11, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammeberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT FILING DATE: 2004-01-16
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-11

Query Match      100.0%; Score 96; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. NO. 9.4e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 IDGQKVDQEPFGHGLVQK 18
Db      1 IDGQKVDQEPFGHGLVQK 18

RESULT 2
US-10-052-788-5
; Sequence 5, Application US/10052788
; Publication No. US20030087314A1
; GENERAL INFORMATION:
; APPLICANT: Gershwin, Laurel J.
; APPLICANT: Pettigrew, Howard David
; APPLICANT: Kalina, Warren V.
; TITLE OF INVENTION: Bepion Immunoglobulin Chain Derived Peptides for
; FILE REFERENCE: 023070-121000US
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: Description of Artificial Sequence:epitope peptide  
OTHER INFORMATION: ps, middle portion of C2 of equine IGE epsilon  
OTHER INFORMATION: heavy chain  
US-10-052-788-5

Query Match 81.2%; Score 78; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 7,4e-06;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 IDGQKVDQFPQHG 14  
Db 2 IDGQKVDQFPQHG 15

## RESULT 3

US-09-880-748-2449  
Sequence 2449, Application US/09880748  
Publication No. US2003005937A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PFS23  
CURRENT APPLICATION NUMBER: US/09/880,748  
CURRENT FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-15  
PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
NUMBER OF SEQ ID NOS: 3239  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2449  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-880-748-2449

Query Match 37.5%; Score 36; DB 3; Length 14;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 FPOHGL 15  
Db 7 FPOHGL 12

## RESULT 4

US-10-293-418-2449  
Sequence 2449, Application US/10293418  
Publication No. US200302396A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PFS23P2  
CURRENT APPLICATION NUMBER: US/10/293,418  
CURRENT FILING DATE: 2002-11-27  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/240,816  
PRIOR FILING DATE: 2000-10-17  
PRIOR APPLICATION NUMBER: 60/212,210  
PRIOR FILING DATE: 2000-06-16  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 2449  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-293-418-2449

Query Match 37.5%; Score 36; DB 4; Length 14;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 FPOHGL 15  
Db 7 FPOHGL 12

## RESULT 5

US-11-054-515-2449  
Sequence 2449, Application US/11054515  
Publication No. US2005025532A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys  
FILE REFERENCE: PFS23P3  
CURRENT APPLICATION NUMBER: US/11/054,515  
CURRENT FILING DATE: 2005-02-10  
PRIOR APPLICATION NUMBER: 60/543,296  
PRIOR FILING DATE: 2004-02-11  
PRIOR APPLICATION NUMBER: 60/580,347  
PRIOR FILING DATE: 2004-06-18  
PRIOR APPLICATION NUMBER: 10/293,418  
PRIOR FILING DATE: 2002-11-14  
PRIOR APPLICATION NUMBER: 60/331,469  
PRIOR FILING DATE: 2001-11-16  
PRIOR APPLICATION NUMBER: 60/340,817  
PRIOR FILING DATE: 2001-12-19  
PRIOR APPLICATION NUMBER: 09/880,748  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/293,499  
PRIOR FILING DATE: 2001-05-25  
PRIOR APPLICATION NUMBER: 60/277,379  
PRIOR FILING DATE: 2001-03-21  
PRIOR APPLICATION NUMBER: 60/276,248  
PRIOR FILING DATE: 2001-03-16  
PRIOR APPLICATION NUMBER: 60/240,816  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 3247  
SEQ ID NO 2449  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-054-515-2449

Query Match 37.5%; Score 36; DB 6; Length 14;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 FPOHGL 15  
Db 7 FPOHGL 12

## RESULT 6

US-11-266-444-2449  
Sequence 2449, Application US/11266444  
Publication No. US20060062789A1  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.

```

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulad
; FILE REFERENCE: PFS2P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2449
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-266-444-2449

Query Match      37.5%; Score 36; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 63;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 FPGHGL 15
      |||||
Db      7 FPGHGL 12

RESULT 7
US-10-758-165-10
; Sequence 10, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammetberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Felis catus
; US-10-758-165-10

Query Match      36.5%; Score 35; DB 5; Length 18;
Best Local Similarity 44.4%; Pred. No. 1.2e+02;
Matches      8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy      1 IDGQVDEQFPQHGIVKQ 18
      :|||:|
Db      1 VDGQKATNIFPYTAPGKQ 18

RESULT 8
US-10-141-627-11
; Sequence 11, Application US/10141627
; Publication No. US2002017663A1
; GENERAL INFORMATION:
; APPLICANT: Dale, James B.
; TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
; FILE REFERENCE: 48112.404C3
; CURRENT APPLICATION NUMBER: US/10/141,627
; CURRENT FILING DATE: 2002-05-07
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; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NH2-terminal fragment of M protein for
; OTHER INFORMATION: constructing antigens, which elicit opsonic
; US-10-141-627-11

Query Match      35.4%; Score 34; DB 4; Length 15;
Best Local Similarity 41.7%; Pred. No. 1.5e+02;
Matches      5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      2 DGQKYDEQFPQKH 13
      |:|:|:|
Db      1 DARSVNGEPPRH 12

RESULT 9
US-10-356-257-255
; Sequence 255, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: Fv1a Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 255
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; US-10-356-257-255

Query Match      35.4%; Score 34; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches      5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      3 GQKYDEQFPQ 12
      |:|:|:|
Db      1 GEQVEEPPE 10

RESULT 10
US-10-758-165-9
; Sequence 9, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammetberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-10-758-165-9

Query Match      35.4%; Score 34; DB 5; Length 18;
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Best Local Similarity 54.5%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 IDGQKVDQFP 11  
: ||| :  
Db 1 VDGQKATNIFP 11

## RESULT 11

US-11-127-804-9  
; Sequence 9, Application US/11127804  
; Publication No. US2006003940A1  
; GENERAL INFORMATION:  
; APPLICANT: Lin, Rong-Hwa  
; TITLE OF INVENTION: T-CELL DEATH-INDUCING EPITOPES  
; FILE REFERENCE: 113062-009001  
; CURRENT APPLICATION NUMBER: US/11/127,804  
; CURRENT FILING DATE: 2005-05-11  
; PRIOR APPLICATION NUMBER: US 60/570,161  
; PRIOR FILING DATE: 2004-05-11  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetically generated peptide  
US-11-127-804-9

Query Match 34.4%; Score 33; DB 6; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.8e+02;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 3 GQKVDQFPQHG 14  
: ||| :  
Db 2 GQKVDQFPQHG 13

RESULT 12  
US-10-079-709-3  
; Sequence 3, Application US/10079709  
; Publication No. US20030119163A1  
; GENERAL INFORMATION:  
; APPLICANT: Robert F.M. Van Gorcom  
; APPLICANT: Willem Van Hartingsveldt  
; APPLICANT: Petrus A. Van Paridon  
; APPLICANT: Annemarie E. Veenstra  
; APPLICANT: Rudolf G.M. Luttin  
; APPLICANT: Gerardus Selden  
; TITLE OF INVENTION: Cloning and Expression of Microbial  
; TITLE OF INVENTION: Phylase  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 545 Middlefield Road, Suite 200  
CITY: Menlo Park  
STATE: California  
COUNTRY: USA  
ZIP: 94025-3471  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/079,709  
FILING DATE: 02-FEB-2002  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/233,510

FILING DATE: 20-JAN-1999  
APPLICATION NUMBER: 07/688,578  
FILING DATE: 24-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 24615-20026.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-327-7250  
TELEFAX: 415-327-2951

INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
FRAGMENT TYPE: N-terminal  
US-10-079-709-3

Query Match 33.3%; Score 32; DB 4; Length 10;  
Best Local Similarity 66.7%; Pred. No. 2e+02;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 VDEQFPQHG 14  
: ||| :  
Db 2 VDERFPYTG 10

RESULT 13  
US-11-036-272-3  
; Sequence 3, Application US/11036272  
; Publication No. US20060063243A1  
; GENERAL INFORMATION:  
; APPLICANT: Robert F.M. Van Gorcom  
; APPLICANT: Willem Van Hartingsveldt  
; APPLICANT: Petrus A. Van Paridon  
; APPLICANT: Annemarie E. Veenstra  
; APPLICANT: Rudolf G.M. Luttin  
; APPLICANT: Gerardus Selden  
; TITLE OF INVENTION: Cloning and Expression of Microbial  
; TITLE OF INVENTION: Phylase  
; NUMBER OF SEQUENCES: 52  
; CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 545 Middlefield Road, Suite 200  
CITY: Menlo Park  
STATE: California  
COUNTRY: USA  
ZIP: 94025-3471  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
SOFTWARE:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/036,272  
FILING DATE: 14-JAN-2005  
CLASSIFICATION:  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/11/036,272  
FILING DATE: 20-JAN-1999  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/688,578  
FILING DATE: 24-MAY-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Murashige, Kate H.  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 24615-20026.00  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-327-7250  
TELEFAX: 415-327-2951



```
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   HYPOTHEICAL: NO
;   FRAGMENT TYPE: N-terminal
US-11-036-272-3
```

```
Query Match      33.3%; Score 32; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
QY      6 VDEQFPQHG 14
      |||:|
Db      2 VDERFPYTG 10
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```
RESULT 14
US-09-880-748-2446
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```
; Sequence 2446, Application US/09880748
; Publication No. US2003005937A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Ruben et al.
```

```
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
```

```
; FILE REFERENCE: PP523
```

```
; CURRENT APPLICATION NUMBER: US/09/880,748
```

```
; CURRENT FILING DATE: 2001-06-15
```

```
; PRIOR APPLICATION NUMBER: 60/212,210
```

```
; PRIOR FILING DATE: 2000-06-15
```

```
; PRIOR APPLICATION NUMBER: 60/240,816
```

```
; PRIOR FILING DATE: 2000-10-17
```

```
; PRIOR APPLICATION NUMBER: 60/276,248
```

```
; PRIOR FILING DATE: 2001-03-16
```

```
; PRIOR APPLICATION NUMBER: 60/277,379
```

```
; PRIOR FILING DATE: 2001-03-21
```

```
; PRIOR APPLICATION NUMBER: 60/293,499
```

```
; PRIOR FILING DATE: 2001-05-25
```

```
; NUMBER OF SEQ ID NOS: 3239
```

```
; SOFTWARE: Patentln Ver. 2.0
```

```
; SEQ ID NO 2446
```

```
; LENGTH: 14
```

```
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
```

```
US-09-880-748-2446
```

```
Query Match      33.3%; Score 32; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      10 FPQHG 14
      |||
Db      7 FPQHG 11
```

```
RESULT 15
US-09-880-748-2703
```

```
; Sequence 2703, Application US/09880748
; Publication No. US2003005937A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Ruben et al.
```

```
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
```

```
; FILE REFERENCE: PP523
```

```
; CURRENT APPLICATION NUMBER: US/09/880,748
```

```
; CURRENT FILING DATE: 2001-06-15
```

```
; PRIOR APPLICATION NUMBER: 60/212,210
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```
; PRIOR FILING DATE: 2000-06-15
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```
; PRIOR APPLICATION NUMBER: 60/240,816
```

```
; PRIOR FILING DATE: 2000-10-17
```

```
; PRIOR APPLICATION NUMBER: 60/276,248
```

```
; PRIOR FILING DATE: 2001-03-16
```

```
; PRIOR APPLICATION NUMBER: 60/277,379
```

```
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2703
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; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2703
```

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Query Match      33.3%; Score 32; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY      10 FPQHG 14
      |||
Db      7 FPQHG 11
```

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Job time : 50.3333 secs
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## OM protein - protein search, using sw model

Run on: May 30, 2006, 15:17:53 ; Search time 4 Seconds  
(without alignments)  
50.118 Million cell updates/sec

Title: US-10-758-165A-11

Perfect score: 96

Sequence: 1 IDGQKVDKDEPPQHGVLKQ 18

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 11661

Minimum DB seq length: 0  
Maximum DB seq length: 18Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database : Published Applications AA New:\*

1: /EMC\_Celerra\_SIDS3/prodata/1/pubppa/US09\_NEW\_PUB pep:\*\n2: /EMC\_Celerra\_SIDS3/prodata/1/pubppa/US06\_NEW\_PUB pep:\*\n3: /EMC\_Celerra\_SIDS3/prodata/1/pubppa/US07\_NEW\_PUB pep:\*\n4: /EMC\_Celerra\_SIDS3/prodata/1/pubppa/US08\_NEW\_PUB pep:\*\n5: /EMC\_Celerra\_SIDS3/prodata/1/pubppa/PCT\_NEW\_PUB pep:\*\n6: /EMC\_Celerra\_SIDS3/prodata/1/pubppa/US10\_NEW\_PUB pep:\*\n7: /EMC\_Celerra\_SIDS3/prodata/1/pubppa/US11\_NEW\_PUB pep:\*\n8: /EMC\_Celerra\_SIDS3/prodata/1/pubppa/US60\_NEW\_PUB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	30.2	9	7	US-11-332-378-136
2	29	30.2	15	7	US-11-140-487A-2148
3	28	29.2	15	6	US-10-544-499-3
4	26	27.1	16	7	US-11-281-644A-2
5	25	26.0	10	7	US-11-122-986-795
6	25	26.0	14	7	US-11-301-554-2108
7	25	26.0	16	6	US-10-522-356-9
8	25	26.0	17	7	US-11-244-348A-7
9	24	25.0	9	7	US-11-332-378-216
10	23	24.0	9	7	US-11-140-487A-794
11	23	24.0	10	7	US-11-140-487A-795
12	23	24.0	10	7	US-11-140-487A-1029
13	23	24.0	14	7	US-11-122-986-542
14	22	22.9	9	7	US-11-122-986-789
15	22	22.9	11	7	US-11-122-986-673
16	22	22.9	15	6	US-10-490-949-35
17	22	22.9	15	6	US-10-543-587-10
18	22	22.9	17	7	US-11-297-317-23
19	22	22.9	18	7	US-11-213-668-90
20	21	21.9	10	6	US-10-538-066-557
21	21	21.9	10	7	US-11-140-487A-990
22	21	21.9	11	6	US-10-538-066-588
23	21	21.9	12	1	US-09-784-950-9
24	21	21.9	13	6	US-10-538-066-589
25	21	21.9	14	7	US-11-219-563-38

26	21	21.9	15	7	US-11-118-324-4	Sequence 4, Appl1
27	21	21.9	17	7	US-11-122-986-398	Sequence 398, App
28	20	20.8	7	7	US-11-122-986-669	Sequence 669, App
29	20	20.8	8	6	US-10-546-594-38	Sequence 38, Appl1
30	20	20.8	9	6	US-10-538-066-326	Sequence 326, App
31	20	20.8	9	6	US-10-538-066-346	Sequence 346, App
32	20	20.8	9	7	US-11-054-072-89	Sequence 89, Appl1
33	20	20.8	9	7	US-11-140-487A-1608	Sequence 1608, App
34	20	20.8	9	7	US-11-167-773-83	Sequence 83, Appl1
35	20	20.8	9	7	US-11-332-378-59	Sequence 59, Appl1
36	20	20.8	9	7	US-11-332-378-63	Sequence 63, Appl1
37	20	20.8	10	6	US-10-538-066-131	Sequence 131, App
38	20	20.8	10	6	US-10-538-066-132	Sequence 132, App
39	20	20.8	10	6	US-10-538-066-328	Sequence 328, App
40	20	20.8	10	6	US-10-538-066-348	Sequence 348, App
41	20	20.8	10	6	US-10-538-066-394	Sequence 394, App
42	20	20.8	10	7	US-11-219-563-16	Sequence 16, Appl1
43	20	20.8	10	7	US-11-140-487A-1506	Sequence 1506, App
44	20	20.8	10	7	US-11-122-986-622	Sequence 622, App
45	20	20.8	10	7	US-11-332-378-60	Sequence 60, Appl1

## ALIGNMENTS

RESULT 1  
US-11-332-378-136  
Sequence 136, Application US/11332378  
Publication No. US20060106196A1  
GENERAL INFORMATION:  
APPLICANT: Gaubert, Gustav  
APPLICANT: Erikson, Jon Amund  
APPLICANT: Moller, Mona  
APPLICANT: Giersten, Marianne Klomp  
APPLICANT: Saetvedal, Ingvald  
APPLICANT: Saetvedal, Ingvald  
TITLE OF INVENTION: Antigenic Peptides Derived from Telomerase  
FILE REFERENCE: 01702.401800  
CURRENT APPLICATION NUMBER: US/11/332.378  
CURRENT FILING DATE: 2006-01-17  
PRIOR APPLICATION NUMBER: US/09/743, 281  
PRIOR FILING DATE: 2001-07-05  
PRIOR APPLICATION NUMBER: PCT/NO99/00220  
PRIOR FILING DATE: 1999-06-30  
NUMBER OF SEQ ID NOS: 231  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 136  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens, other or unknown  
US-11-332-378-136  
Query Match 30.2%; Score 29; DB 7; Length 9;  
Best Local Similarity 71.4%; Pred. No. 5.2e+04;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 9 QPQHG 15  
DB 3 QMPAHL 9  
RESULT 2  
US-11-140-487A-2148  
Sequence 2148, Application US/11140487A  
Publication No. US20060093617A1  
GENERAL INFORMATION:  
APPLICANT: Immunogenetics N.V.  
TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C virus  
FILE REFERENCE: 166  
CURRENT APPLICATION NUMBER: US/11/140.487A  
CURRENT FILING DATE: 2005-05-31  
PRIOR APPLICATION NUMBER: EP 04012951.2  
PRIOR FILING DATE: 2004-06-01

PRIOR APPLICATION NUMBER: EP 04447239.7  
PRIOR FILING DATE: 2004-10-28  
PRIOR APPLICATION NUMBER: EP 05102441.2  
PRIOR FILING DATE: 2005-03-25  
PRIOR APPLICATION NUMBER: US 60/576,310  
PRIOR FILING DATE: 2004-06-03  
PRIOR APPLICATION NUMBER: US 60/622,782  
PRIOR FILING DATE: 2004-10-29  
PRIOR APPLICATION NUMBER: US 60/665,395  
PRIOR FILING DATE: 2005-03-25  
NUMBER OF SEQ ID NOS: 2278  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2148  
LENGTH: 15  
TYPE: PRT  
ORGANISM: hepatitis C virus  
US-11-140-487A-2148

Query Match 30.2%; Score 29; DB 7; Length 15;  
Best Local Similarity 46.2%; Pred. No. 27;  
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GQKVDQFPQHG 15  
Db 1 GMDLAQFKQKAL 13

RESULT 3  
US-10-544-499-3  
Sequence 3, Application US/10544499  
Publication No. US2006094017A1  
GENERAL INFORMATION:  
APPLICANT: Anthony J. Conley  
APPLICANT: Beverly H. Gallinski  
APPLICANT: Allison Montalvo  
TITLE OF INVENTION: Immunogens for HIV Vaccine  
FILE REFERENCE: 21219P  
CURRENT APPLICATION NUMBER: US/10/544,499  
CURRENT FILING DATE: 2005-08-03  
PRIOR APPLICATION NUMBER: 60/447,590  
PRIOR FILING DATE: 2003-02-14  
PRIOR APPLICATION NUMBER: PCT/US04/05821  
PRIOR FILING DATE: 2004-02-10  
NUMBER OF SEQ ID NOS: 7  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic peptide mimotope  
US-10-544-499-3

Query Match 29.2%; Score 28; DB 6; Length 15;  
Best Local Similarity 50.0%; Pred. No. 40;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 9 QPQHGIV 16  
Db 2 KIPDHGIV 9

RESULT 4  
US-11-281-644A-2  
Sequence 2, Application US/11281644A  
Publication No. US20060105953A1  
GENERAL INFORMATION:  
APPLICANT: Arnaud Lacoste  
APPLICANT: Christopher J. Evans  
TITLE OF INVENTION: SYSTEM FOR PROTEASE MEDIATED PROTEIN  
FILE REFERENCE: 30435.164-US-UI  
CURRENT APPLICATION NUMBER: US/11/281,644A

CURRENT FILING DATE: 2005-11-17  
PRIOR APPLICATION NUMBER: 60/628,694  
PRIOR FILING DATE: 2004-11-17  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide linker  
US-11-281-644A-2

Query Match 27.1%; Score 26; DB 7; Length 16;  
Best Local Similarity 57.1%; Pred. No. 93;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IDGQKVD 7  
Db 4 VDGDQVD 10

RESULT 5  
US-11-122-986-795  
Sequence 795, Application US/11122986  
Publication No. US20060104989A1  
GENERAL INFORMATION:  
APPLICANT: DHARMSI, ALD  
APPLICANT: VEDADI, MASOUD  
TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES  
FILE REFERENCE: IPT-330.01  
CURRENT APPLICATION NUMBER: US/11/122,986  
CURRENT FILING DATE: 2005-05-05  
PRIOR APPLICATION NUMBER: 60/423,875  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: 60/423,832  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: 60/423,915  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: 60/423,757  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: 60/423,758  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: 60/424,367  
PRIOR FILING DATE: 2002-11-06  
PRIOR APPLICATION NUMBER: 60/424,376  
PRIOR FILING DATE: 2002-11-06  
PRIOR APPLICATION NUMBER: 60/424,370  
PRIOR FILING DATE: 2002-11-06  
PRIOR APPLICATION NUMBER: 60/424,362  
PRIOR FILING DATE: 2002-11-06  
PRIOR APPLICATION NUMBER: 60/424,373  
PRIOR FILING DATE: 2002-11-06  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 844  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 795  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Streptococcus pneumoniae  
US-11-122-986-795

Query Match 26.0%; Score 25; DB 7; Length 10;  
Best Local Similarity 62.5%; Pred. No. 81;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 FPGHGLVK 17  
Db 3 FPEVGLKK 10

RESULT 6

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US-11-301-554-2108
; Sequence 2108, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Matanabe, Yoshinhiro
; APPLICANT: Kaios, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Derrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedavick, Thomas S.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Mcnabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT FILING DATE: 2005-12-13
; PRIOR FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2108
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-301-554-2108

Query Match      26.0%; Score 25; DB 7; Length 14;
Best Local Similarity 45.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 IDGQVDEQFP 11
       |:|:|
Db      2 IERRKIMEQSP 12

RESULT 7
US-10-522-356-9
; Sequence 9, Application US/10522356
; Publication No. US20060105323A1
; GENERAL INFORMATION:
; APPLICANT: WHITELEW, CHRISTOPHER BRUCE ALEXANDER
; APPLICANT: CLARK, ANTHONY JOHN
; APPLICANT: WOLF, CHARLES ROLAND
; TITLE OF INVENTION: MULTI-REPORTER GENE MODEL FOR TOXICOLOGICAL SCREENING
; FILE REFERENCE: 102286.155 US1
; CURRENT APPLICATION NUMBER: US/10/522,356
; PRIOR FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: PCT/GB03/003192
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; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: GB 0217402.7
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Sequence: ARF
; OTHER INFORMATION: epitope from unknown organism
US-10-522-356-9

Query Match      26.0%; Score 25; DB 6; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      8 EQFPQH 13
       |:|
Db      8 ERFPQH 13

RESULT 8
US-11-244-348A-7
; Sequence 7, Application US/11244348A
; Publication No. US2006010493A1
; GENERAL INFORMATION:
; APPLICANT: Mreny, Randall J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IMMUNIZING
; TITLE OF INVENTION: AGAINST PSEUDOMONAS INFECTION
; FILE REFERENCE: 10901-015-999
; CURRENT APPLICATION NUMBER: US/11/244,348A
; CURRENT FILING DATE: 2005-10-04
; PRIOR APPLICATION NUMBER: 60/616,125
; PRIOR FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Pseudomonas sp.
US-11-244-348A-7

Query Match      26.0%; Score 25; DB 7; Length 17;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY      7 DEQFPQHGLVK 17
       |:|:|
Db      7 DEQFIPKGCCK 17

RESULT 9
US-11-332-378-216
; Sequence 216, Application US/11332378
; Publication No. US20060106196A1
; GENERAL INFORMATION:
; APPLICANT: Gaudernack, Gustav
; APPLICANT: Eriksen, Jon Amund
; APPLICANT: Moller, Mona
; APPLICANT: Gjertsen, Marianne Klemp
; APPLICANT: Saeterdal, Ingvil
; APPLICANT: Saebøe-Larsen, Stein
; TITLE OF INVENTION: Antigenic Peptides Derived from Telomerase
; FILE REFERENCE: 01702.401800
; CURRENT APPLICATION NUMBER: US/11/332,378
; CURRENT FILING DATE: 2006-01-17
; PRIOR APPLICATION NUMBER: US/09/743,281
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: PCT/NO99/00220
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 231
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```
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 216
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens, other or unknown
US-11-332-378-216
```

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Query Match          25.0%; Score 24; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.2e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

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QY          11 EQFPQHGL 15
Db          2 EQFKQKAL 6
```

```
RESULT 10
US-11-140-487A-794
; Sequence 794, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 794
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-794
```

```
Query Match          24.0%; Score 23; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5.2e+04;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY          8 EQFPQHGL 15
Db          2 EQFKQKAL 9
```

```
RESULT 11
US-11-140-487A-795
; Sequence 795, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
```

```
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 795
; LENGTH: 10
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-795
```

```
Query Match          24.0%; Score 23; DB 7; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY          8 EQFPQHGL 15
Db          2 EQFKQKAL 9
```

```
RESULT 12
US-11-140-487A-1029
; Sequence 1029, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1029
; LENGTH: 10
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-1029
```

```
Query Match          24.0%; Score 23; DB 7; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY          8 EQFPQHGL 15
Db          1 EQFKQKAL 8
```

```
RESULT 13
US-11-122-986-542
; Sequence 542, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
```

```
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; PRIOR FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
```

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; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: Patentln Ver. 3.3
; SEQ ID NO 542
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-11-122-986-542

```

```

Query March 24.0%; Score 23; DB 7; Length 14;
Best Local Similarity 30.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 4 QKVDQEPFH 13
:::|:|
Db 1 EELDDAFDYH 10

```

```

RESULT 14
US-11-122-986-789
; Sequence 789, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARWASTI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; PRIOR FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: Patentln Ver. 3.3
; SEQ ID NO 789

```

```

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-11-122-986-789

```

```

Query March 22.9%; Score 22; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.2e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 10 FPGHGL 15
:::|:|
Db 3 FPEVGL 8

```

```

RESULT 15
US-11-122-986-673
; Sequence 673, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARWASTI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; PRIOR FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: Patentln Ver. 3.3
; SEQ ID NO 673
; LENGTH: 11;
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-11-122-986-673

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```

Query March 22.9%; Score 22; DB 7; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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QY 3 GQKVDQEPQ 12
:::|:|
Db 2 GKLDDEDMFR 11

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Job time : 4 secs

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OM protein - protein search, using sw model

Run on: May 30, 2006, 15:08:01 ; Search time 19.3333 Seconds  
(without alignments)  
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Title: US-10-758-165A-11  
Perfect score: 96  
Sequence: 1 IDGQKVDGEPFGHGVKQ 18

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Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 271358

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /EMC\_Celerra\_SIDS3/prodata/2/iaa/7 COMB.pep.\*  
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7: /EMC\_Celerra\_SIDS3/prodata/2/iaa/bocfile1.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	35.4	15	2	US-08-914-479A-11 Sequence 11, Appl
2	32	33.3	10	1	US-08-151-574-3 Sequence 3, Appl
3	32	33.3	10	1	US-08-419-448-3 Sequence 3, Appl
4	32	33.3	10	2	US-09-233-510-3 Sequence 3, Appl
5	30	31.2	11	1	US-08-486-839-8 Sequence 8, Appl
6	30	31.2	11	2	US-09-151-011-8 Sequence 8, Appl
7	30	31.2	11	2	US-09-343-623-8 Sequence 8, Appl
8	30	31.2	11	2	US-09-977-827-8 Sequence 8, Appl
9	29	30.2	9	3	US-09-743-281C-136 Sequence 136, App
10	29	30.2	10	1	US-08-166-195A-23 Sequence 23, Appl
11	29	30.2	10	1	US-08-436-772-23 Sequence 23, Appl
12	29	30.2	10	1	US-08-436-883B-23 Sequence 23, Appl
13	29	30.2	11	1	US-08-486-839-12 Sequence 12, Appl
14	29	30.2	11	2	US-09-151-011-12 Sequence 12, Appl
15	29	30.2	11	2	US-09-343-623-12 Sequence 12, Appl
16	29	30.2	11	2	US-09-977-827-13 Sequence 13, Appl
17	29	30.2	11	2	US-09-977-827-13 Sequence 13, Appl
18	29	30.2	16	2	US-09-511-625B-64 Sequence 64, Appl
19	28	29.2	15	1	US-07-995-503A-10 Sequence 10, Appl
20	28	29.2	15	1	US-08-390-790-10 Sequence 10, Appl
21	28	29.2	15	1	US-08-390-790-10 Sequence 10, Appl
22	28	29.2	15	1	US-08-390-509-10 Sequence 10, Appl
23	28	29.2	15	2	US-09-149-860A-10 Sequence 10, Appl
24	28	29.2	17	2	US-08-836-561-41 Sequence 41, Appl
25	28	29.2	17	2	US-09-434-122-41 Sequence 41, Appl
26	27	28.1	10	2	US-08-371-680-10 Sequence 10, Appl

ALIGNMENTS

27	27	28.1	11	1	US-08-486-839-14	Sequence 14, Appl
28	27	28.1	11	2	US-09-151-011-14	Sequence 14, Appl
29	27	28.1	11	2	US-09-343-623-14	Sequence 14, Appl
30	27	28.1	11	2	US-09-977-827-15	Sequence 15, Appl
31	27	28.1	15	2	US-08-475-955-75	Sequence 75, Appl
32	27	28.1	15	2	US-07-867-819D-75	Sequence 107, App
33	27	28.1	16	2	US-09-701-588C-107	Sequence 13, Appl
34	26	27.1	11	1	US-08-486-839-13	Sequence 13, Appl
35	26	27.1	11	2	US-09-151-011-13	Sequence 13, Appl
36	26	27.1	11	2	US-09-343-623-13	Sequence 13, Appl
37	26	27.1	11	2	US-09-685-010-19	Sequence 14, Appl
38	26	27.1	11	2	US-09-977-827-14	Sequence 14, Appl
39	26	27.1	11	2	US-09-978-309A-49	Sequence 49, Appl
40	26	27.1	11	2	US-09-978-309A-84	Sequence 84, Appl
41	26	27.1	12	1	US-08-151-574-9	Sequence 9, Appl
42	26	27.1	12	1	US-08-196-940-3	Sequence 9, Appl
43	26	27.1	12	1	US-08-419-448-9	Sequence 9, Appl
44	26	27.1	12	2	US-09-233-510-9	Sequence 12, Appl
45	26	27.1	12	2	US-09-685-010-12	Sequence 12, Appl

RESULT 1  
US-08-914-479A-11  
Sequence 11, Application US/08914479A  
Patent No. 6419932  
GENERAL INFORMATION:  
APPLICANT: Dale, James B.  
TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER  
FILE REFERENCE: 481112.404C2  
CURRENT FILING DATE: 1997-08-19  
PRIOR APPLICATION NUMBER: 08/409,270  
PRIOR FILING DATE: 1995-03-23  
PRIOR APPLICATION NUMBER: 07/945,860  
PRIOR FILING DATE: 1992-09-16  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: NH2-terminal fragment of M protein for  
OTHER INFORMATION: constructing antigen, which elicit opsonic  
OTHER INFORMATION: antibodies in an immunized animal  
US-08-914-479A-11  
Query Match 35.4%; Score 34; DB 2; Length 15;  
Best Local Similarity 41.7%; Pred. No. 27;  
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
QY 2 DGQKVDGEPFGH 13  
Db 1 DARSNGEPPRH 12  
US-08-151-574-3  
Sequence 3, Application US/08151574  
Patent No. 5436156  
GENERAL INFORMATION:  
APPLICANT: Robert F.M. Van Gorcom  
APPLICANT: Willem Van Hartingsveldt  
APPLICANT: Petrus A. Van Paridon  
APPLICANT: Annemarie E. Veenstra  
APPLICANT: Rudolf G.M. Luttin  
TITLE OF INVENTION: Cloning and Expression of Microbial  
TITLE OF INVENTION: Phytase

```

1 NUMBER OF SEQUENCES: 52
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: Morrison & Foerster
4 STREET: 545 Middlefield Road, Suite 200
5 CITY: Menlo Park
6 STATE: California
7 COUNTRY: USA
8 ZIP: 94025-3471
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: Floppy disk
12 COMPUTER: IBM PC compatible
13 OPERATING SYSTEM: PC-DOS/MS-DOS
14 SOFTWARE: Patentin Release #1.0, Version #1.25
15
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/08/151,574
18 FILING DATE:
19 CLASSIFICATION: 435
20 PRIOR APPLICATION DATA:
21 APPLICATION NUMBER: 07/688,578
22 FILING DATE: 24-MAY--1991
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Murashige, Kate H.
25 REGISTRATION NUMBER: 29,959
26 REFERENCE/DOCKET NUMBER: 24615-20026.00
27 TELECOMMUNICATION INFORMATION:
28 TELEPHONE: 415-337-7250
29
30 INFORMATION FOR SEQ ID NO: 3:
31 SEQUENCE CHARACTERISTICS:
32 LENGTH: 10 amino acids
33 TYPE: amino acid
34 TOPOLOGY: linear
35 MOLECULE TYPE: peptide
36 HYPOTHEetical: NO
37 FRAGMENT TYPE: N-terminal
38
39 US-08-151-574-3
40
41 Query Match 33.3% Score 32; DB 1; Length 10;
42 Best Local Similarity 66.7% Pred. No. 38;
43 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
44
45 QY 6 VDEQPHNG 14
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48 Db 2 VDERFPYTG 10
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: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/419,448
: FILING DATE: 10-APR-1995
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Murashige, Kate H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 24615-20026.10
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-887-1500
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: HYPOTHEICAL: NO
: FRAGMENT TYPE: N-terminal
US-08-419-448-3

Query Match      33.3%; Score 32; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 2; Gaps 0;

Qy      6 VDEQFPQHG 14
      |||:| |
Db      2 VDERFPYTG 10

RESULT 4
US-09-233-510-3
: Sequence 3, Application US/09233510
: Patent No. 6350602
: GENERAL INFORMATION:
: APPLICANT: Robert F.M. Van Gorcom
: APPLICANT: Willem Van Hartingsveldt
: APPLICANT: Petrus A. Van Paridon
: APPLICANT: Annemarie E. Veenstra
: APPLICANT: Rudolf G.M. Luttin
: APPLICANT: Gerardus Sellen
: TITLE OF INVENTION: Cloning and Expression of Microbial
: TITLE OF INVENTION: Phytase
: NUMBER OF SEQUENCES: 52
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Morrison & Foerster
: STREET: 545 Middlefield Road, Suite 200
: CITY: Menlo Park
: STATE: California
: COUNTRY: USA
: ZIP: 94025-3471
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: SOFTWARE:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/233,510
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/688,578
: FILING DATE: 24-MAY-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Murashige, Kate H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 24615-20026.00
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-327-7250
: TELEFAX: 415-327-2951
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 10 amino acids

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TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
FRAGMENT TYPE: N-terminal  
US-09-233-510-3

Query Match 33.3%; Score 32; DB 2; Length 10;  
Best Local Similarity 66.7%; Pred. No. 38;  
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 VDEQFQHG 14  
Db 2 VDERFPYTG 10

RESULT 5  
US-08-486-839-8  
Sequence 8, Application US/08486839  
Patent No. 5928928  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: A human chitinase, its recombinant  
TITLE OF INVENTION: production, its use for decomposing chitin, its use  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann & Baron  
STREET: 350 Jericho Turnpike  
CITY: Jericho  
STATE: New York  
COUNTRY: United States of America  
ZIP: 11758  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,839  
FILING DATE: 07 - June - 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Baton, Ronald J.  
REGISTRATION NUMBER: 29,281  
REFERENCE/DOCKET NUMBER: 294-26  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 822-3550  
TELEFAX: (516) 822-3582  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
US-08-486-839-8

Query Match 31.2%; Score 30; DB 1; Length 11;  
Best Local Similarity 50.0%; Pred. No. 93;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DGQKVDQFP 11  
Db 2 DGVDWDFP 11

RESULT 6  
US-09-151-011-8  
Sequence 8, Application US/09151011  
Patent No. 6057142  
GENERAL INFORMATION:

APPLICANT:  
TITLE OF INVENTION: A Human Chitinase, Its Recombinant  
TITLE OF INVENTION: Production, Its Use For Decomposing Chitin, Its Use in  
TITLE OF INVENTION: Therapy or Prophylaxis Against Infection Diseases.  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann & Baron, LLP  
STREET: 6900 Jericho Turnpike  
CITY: Syosset  
STATE: New York  
COUNTRY: United States of America  
ZIP: 11791  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/151,011  
FILING DATE: 10 - September - 1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Morris, Robert C.  
REGISTRATION NUMBER: 42,910  
REFERENCE/DOCKET NUMBER: 294-32 DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 822-3550  
TELEFAX: (516) 822-3582  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
US-09-151-011-8

Query Match 31.2%; Score 30; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 93;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DGQKVDQFP 11  
Db 2 DGVDWDFP 11

RESULT 7  
US-09-343-623-8  
Sequence 8, Application US/09343623  
Patent No. 6303118  
GENERAL INFORMATION:  
APPLICANT:  
TITLE OF INVENTION: A human chitinase, its recombinant  
TITLE OF INVENTION: production, its use for decomposing chitin, its use  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hoffmann & Baron  
STREET: 350 Jericho Turnpike  
CITY: Jericho  
STATE: New York  
COUNTRY: United States of America  
ZIP: 11758  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/343,623  
FILING DATE:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/486,839  
FILING DATE: 07-June-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Barton, Ronald J.  
REGISTRATION NUMBER: 29,281  
REFERENCE/DOCKET NUMBER: 294-26  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (516) 822-3550  
TELEFAX: (516) 822-3582  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-09-343-623-8

Query Match 31.2%; Score 30; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 93;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGQKVDQFP 11  
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Db 2 DGVIDWDFP 11

RESULT 8  
US-09-977-827-8  
Sequence 8, Application US/09977827  
Patent No. 6896884  
GENERAL INFORMATION:  
APPLICANT: Aerts, Johannes Maria F.G.  
TITLE OF INVENTION: A human chitinase, its recombinant production, its use for decomp  
TITLE OF INVENTION: chitin, its use in therapy or prophylaxis against infectious dis  
FILE REFERENCE: Docket 294-32 DIVII/CON  
CURRENT APPLICATION NUMBER: US/09/977,827  
CURRENT FILING DATE: 2001-10-15  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 8  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Autographa californica  
US-09-977-827-8

Query Match 31.2%; Score 30; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 93;  
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGQKVDQFP 11  
|||:|:  
Db 2 DGVIDWDFP 11

RESULT 9  
US-09-743-281C-136  
Sequence 136, Application US/09743281C  
Patent No. 7030211  
GENERAL INFORMATION:  
APPLICANT: Gaudernack, Gustav  
APPLICANT: Eriksen, Jon Amund  
APPLICANT: Moller, Mona  
APPLICANT: Gjertsen, Marianne Klomp  
APPLICANT: Sjaeterdal, Ingvil  
APPLICANT: Saebøe-Larsen, Stein  
TITLE OF INVENTION: Antigenic Peptides Derived from Telomerase  
FILE REFERENCE: 01702,401800  
CURRENT APPLICATION NUMBER: US/09/743,281C  
CURRENT FILING DATE: 2001-07-05  
PRIOR APPLICATION NUMBER: PCT/NO99/00220

PRIOR FILING DATE: 1999-06-30  
NUMBER OF SEQ ID NOS: 231  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 136  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens, other or unknown  
US-09-743-281C-136

Query Match 30.2%; Score 29; DB 3; Length 9;  
Best Local Similarity 71.4%; Pred. No. 5e+05;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 QPQHGL 15  
|||:|:  
Db 3 QMPAHGL 9

RESULT 10  
US-08-166-195A-23  
Sequence 23, Application US/08166195A  
Patent No. 5480799  
GENERAL INFORMATION:  
APPLICANT: O'Rand, Michael G.  
APPLICANT: Wiggren, Esther E.  
APPLICANT: Richardson, Richard T.  
APPLICANT: Lea, Isabel  
TITLE OF INVENTION: Sperm Antigen Corresponding to a  
TITLE OF INVENTION: Sperm Zona Binding Protein Autoantigenic Epitope  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kenneth D. Sibley  
STREET: P.O. Box 34009  
CITY: Charlotte  
STATE: No. 5480799ch Carolina  
COUNTRY: USA  
ZIP: 28234  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/166,195A  
FILING DATE: 10 DEC 1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sibley, Kenneth D.  
REGISTRATION NUMBER: 31,665  
REFERENCE/DOCKET NUMBER: 5470/73  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 919-881-3140  
TELEFAX: 919-881-3175  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 10 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-166-195A-23

Query Match 30.2%; Score 29; DB 1; Length 10;  
Best Local Similarity 62.5%; Pred. No. 1.2e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GQKVDQFP 10  
|||:|:  
Db 1 GAKVDQFP 8

RESULT 11  
US-08-436-772-23

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; Sequence 23, Application US/08436772
; Patent No. 5814456
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Wiggren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5814456th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,772
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-73B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-436-772-23

Query Match          30.2%  Score 29; DB 1; Length 10;
Best Local Similarity 62.5%  Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      3 GAKVDEQF 10
Db      1 GAKVDKRF 8

RESULT 12
US-08-436-883B-23
; Sequence 23, Application US/08436883B
; Patent No. 5820861
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Wiggren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5820861th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,883B
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-73C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-436-883B-23

Query Match          30.2%  Score 29; DB 1; Length 10;
Best Local Similarity 62.5%  Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      3 GAKVDEQF 10
Db      1 GAKVDKRF 8

RESULT 13
US-08-486-839-12
; Sequence 12, Application US/08486839
; Patent No. 5928928
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A human chitinase, its recombinant
; TITLE OF INVENTION: production, its use for degrading chitin, its use
; TITLE OF INVENTION: in therapy or prophylaxis against infection diseases.
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11758
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,839
; FILING DATE: 07 - June - 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Baron, Ronald J.
; REGISTRATION NUMBER: 29,281
; REFERENCE/DOCKET NUMBER: 294-26
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-486-839-12
```

Query Match 30.2%; Score 29; DB 1; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGQKVDQFP 11  
 || : ||  
 Db 2 DGLNLDWQYP 11

RESULT 14  
 US-09-151-011-12  
 ; Sequence 12, Application US/09151011  
 ; Patent No. 6057142  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: A Human Chitinase, Its Recombinant  
 ; TITLE OF INVENTION: Production, Its Use For Decomposing Chitin, Its Use in  
 ; TITLE OF INVENTION: Therapy or Prophylaxis Against Infection Diseases.  
 ; NUMBER OF SEQUENCES: 16  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: Hoffmann & Baron, LLP  
 ; STREET: 6900 Jericho Turnpike  
 ; CITY: Syosset  
 ; STATE: New York  
 ; COUNTRY: United States of America  
 ; ZIP: 11791  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ;  
 ; SOFTWARE:  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/151,011  
 ; FILING DATE: 10 - September - 1998  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Morris, Robert C.  
 ; REGISTRATION NUMBER: 42,910  
 ; REFERENCE/DOCKET NUMBER: 294-32 DIV  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (516) 822-3550  
 ; TELEFAX: (516) 822-3582  
 ; INFORMATION FOR SEQ ID NO: 12:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: protein  
 ; HYPOTHEICAL: NO  
 ;  
 ; US-09-151-011-12

Query Match 30.2%; Score 29; DB 2; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGQKVDQFP 11  
 || : ||  
 Db 2 DGLNLDWQYP 11

RESULT 15  
 US-09-343-623-12  
 ; Sequence 12, Application US/09343623  
 ; Patent No. 630318  
 ; GENERAL INFORMATION:  
 ; APPLICANT:  
 ; TITLE OF INVENTION: A human chitinase, its recombinant  
 ; TITLE OF INVENTION: production, its use for decomposing chitin, its use  
 ; TITLE OF INVENTION: in therapy or prophylaxis against infection diseases.  
 ; NUMBER OF SEQUENCES: 16  
 ; CORRESPONDENCE ADDRESSES:  
 ;

ADDRESSEE: Hoffmann & Baron  
 STREET: 350 Jericho Turnpike  
 CITY: Jericho  
 STATE: New York  
 COUNTRY: United States of America  
 ZIP: 11758  
 ;  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ;  
 ; SOFTWARE:  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/343,623  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/486,839  
 ; FILING DATE: 07-June-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Baron, Ronald J.  
 ; REGISTRATION NUMBER: 29,281  
 ; REFERENCE/DOCKET NUMBER: 294-26  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (516) 822-3550  
 ; TELEFAX: (516) 822-3582  
 ; INFORMATION FOR SEQ ID NO: 12:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 11 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: unknown  
 ; TOPOLOGY: unknown  
 ; MOLECULE TYPE: protein  
 ; HYPOTHEICAL: NO  
 ;  
 ; US-09-343-623-12

Query Match 30.2%; Score 29; DB 2; Length 11;  
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;  
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGQKVDQFP 11  
 || : ||  
 Db 2 DGLNLDWQYP 11

Search completed: May 30, 2006, 15:09:24  
 Job time : 19.333 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2006, 15:04:28 ; Search time 12 Seconds  
(without alignments)  
144.325 Million cell updates/sec

Title: US-10-758-165A-10

Perfect score: 97

Sequence: 1 VDCGKATNIPYTPAKQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.80:\*  
2: PIR1:\*  
3: PIR2:\*  
4: PIR3:\*  
5: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	27.8	17	2	H49048
2	27	27.8	18	2	A59137
3	26	26.8	18	2	A61577
4	24	24.7	14	2	B58502
5	24	24.7	17	2	S18534
6	23	23.7	12	2	P00786
7	23	23.7	15	2	B45115
8	23	23.7	18	2	S20322
9	22	22.7	12	2	P01070
10	22	22.7	13	2	S01904
11	22	22.7	15	2	PA0056
12	22	22.7	15	2	PA0087
13	22	22.7	15	2	PA0099
14	22	22.7	16	2	A28144
15	22	22.7	17	2	C4063
16	22	22.7	18	2	C56046
17	21	21.6	10	2	S71948
18	21	21.6	10	2	A39745
19	21	21.6	11	2	A4135
20	21	21.6	12	2	A53524
21	21	21.6	14	2	PU0142
22	21	21.6	14	2	S59495
23	21	21.6	15	2	B61457
24	21	21.6	16	2	B53284
25	21	21.6	16	2	S38292
26	21	21.6	17	2	S50901
27	21	21.6	18	2	S57518
28	21	21.6	18	2	S70612
29	20.5	21.1	18	2	A28027

30	20	20.6	9	2	S59902	glutathione transf
31	20	20.6	9	2	D48186	ATPase R1 subunit
32	20	20.6	9	2	S10784	enamelin 1 - bovin
33	20	20.6	13	2	B58533	CD61 homolog - cha
34	20	20.6	14	2	S22236	lipoxigenase (EC 1
35	20	20.6	14	2	S19803	ubiquitin - potato
36	20	20.6	14	2	PA0109	porin por 1B - Ara
37	20	20.6	14	2	G44957	photosystem II oxy
38	20	20.6	14	2	PH1306	1g heavy chain DU
39	20	20.6	14	2	PA0045	porin por1 - Arabi
40	20	20.6	14	2	S12904	protein kinase (EC
41	20	20.6	15	2	PA0097	starch phosphoryla
42	20	20.6	15	2	S71300	ICL3 protein - Par
43	20	20.6	15	2	PS0455	superoxide dismuta
44	20	20.6	15	2	PA0063	ubiquitin - fungus
45	20	20.6	15	2	A49177	22k protein p1, ml

#### ALIGNMENTS

RESULT 1  
H49048  
T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)  
C.Species: Homo sapiens (man)  
C.Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997  
C.Accession: H49048  
R.Stoud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.  
Eur. J. Immunol. 22, 2413-2418, 1992  
A.Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenile  
A.Reference number: H49048; MUID:92387250; PMID:1387614  
A.Accession: H49048  
A.Status: Preliminary; not compared with conceptual translation  
A.Molecule type: mRNA  
A.Residues: 1-17 <SIO>  
A.Cross-references: UNIPARC:UPI0000176DF0  
A.Note: sequence extracted from patient SS, IL-2R+ syrovial T-cells  
A.Note: sequence extracted from NCBI backbone (NCBI:113270)  
C.Superfamily: Immunoglobulin V region; immunoglobulin homology  
C.Keywords: T-cell receptor

Query Match 27.8% Score 27; DB 2; Length 17;  
Best Local Similarity 62.5%; Pred. No. 3.5e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ATNIPYPT 13  
DB 8 AMTFPPYT 15

RESULT 2  
A59137  
protein p11 - golden needle mushroom (fragment)  
C.Species: Flammulina velutipes (golden needle mushroom)  
C.Date: 12-Nov-1999 #sequence\_revision 12-Nov-1999 #text\_change 09-Jul-2004  
R.Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.  
submitted to the Protein Sequence Database, November 1999  
A.Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr  
A.Reference number: A59137  
A.Accession: A59137  
A.Status: preliminary  
A.Molecule type: protein  
A.Residues: 1-18 <SAK>  
A.Cross-references: UNIPROT:Q7M4W6; UNIPARC:UPI000017CB27

Query Match 27.8% Score 27; DB 2; Length 18;  
Best Local Similarity 80.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 PYTAP 15  
DB 2 PYTSP 6

## RESULT 3

A61577 24k serine proteinase (EC 3.4.21.-) - Streptomyces fradiae (fragment)  
C:Species: Streptomyces fradiae  
C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004  
C:Accession: A61577  
R:Sinha, U.; Molz, S.A.; Lad, P.J.  
Int. J. Biochem. 23, 979-984, 1991  
A:Title: Two new extracellular serine proteases from Streptomyces fradiae.  
A:Reference number: A61577; MUID:92155439; PMID:1786859  
A:Accession: A61577  
A:Molecule type: Protein  
A:Residues: 1-18 <SIN>  
A:Cross-references: UNIPROT:Q7M198; UNIPARC:UPI000017AB13  
C:Keywords: extracellular protein; hydrolase; serine proteinase

## Query Match

Best Local Similarity 26.8%; Score 26; DB 2; Length 18;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 1 VDQKATNIPY 12  
|||  
|:|:|

Db 2 VGTTRAAQEPWP 13

## RESULT 4

B58502 36k kidney stone protein - unidentified bacterium (fragment)  
C:Species: unidentified bacterium  
C:Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998  
C:Accession: B58502  
R:Binette, J.P.; Binette, M.B.  
submitted to the Protein Sequence Database, October 1996  
A:Description: The proteins of kidney and gallbladder stones.  
A:Reference number: A58501  
A:Accession: B58502  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-14 <BIN>  
A:Cross-references: UNIPARC:UPI000017ABD0  
A:Experimental source: human kidney stone containing Ca ox.monoh dihyd, 1% struvite, CaH  
A:Note: tentative identification of 8-Tyr and 9-Thr

## Query Match

Best Local Similarity 24.7%; Score 24; DB 2; Length 14;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 8 NIPPYT 13  
|||  
|:|:|

Db 4 NLFCYT 9

## RESULT 5

S18534 hypothetical protein 7 (eryG 3' region) - Saccharopolyspora erythraea (fragment)  
C:Species: Saccharopolyspora erythraea  
C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 07-Apr-1994  
C:Accession: S18534  
R:Haydock, S.F.; Dowson, J.A.; Dhillon, N.; Roberts, G.A.; Cortes, J.; Leadlay, P.F.  
Mol. Gen. Genet. 230, 120-128, 1991  
A:Title: Cloning and sequence analysis of genes involved in erythromycin biosynthesis in  
methyltransferases  
A:Reference number: S18530; MUID:92079886; PMID:1840640  
A:Accession: S18534  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-17 <HAY>  
A:Cross-references: UNIPARC:UPI000017ADB1; EMBL:X60379  
A:Note: the authors translated the codon CTG for residue 12 as Gly

## Query Match

Best Local Similarity 24.7%; Score 24; DB 2; Length 17;

Best Local Similarity 62.5%; Pred. No. 1.2e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 9 IFPYAPG 16  
|||  
|:|:|

Db 1 IFPAVAG 8

## RESULT 6

P00786 NADH2 dehydrogenase (EC 1.6.99.3) 26k chain - fava bean mitochondrion (fragment)  
N:Alternative names: complex I 26k chain; NADH-ubiquinone reductase 26k chain  
C:Species: mitochondrion Vicia faba (fava bean)  
C:Date: 03-May-1994 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004  
C:Accession: P00786  
R:Letecme, S.; Boulter, M.  
Plant Physiol. 102, 435-443, 1993  
A:Title: Purification and preliminary characterization of mitochondrial complex I (NADH-ubiquinone reductase)  
A:Reference number: P00775; MUID:94151437; PMID:8108509  
A:Accession: P00786  
A:Molecule type: protein  
A:Residues: 1-12 <LET>  
A:Cross-references: UNIPROT:Q7M2G3; UNIPARC:UPI000017CDA8  
C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the th  
ranging from 5K to 75K.  
C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by

C:Genetics:

A:Genome: mitochondrion  
C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 23.7%; Score 23; DB 2; Length 12;  
Best Local Similarity 53.8%; Pred. No. 1.2e+03;

Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

Oy 6 ATNI-FPYAPGK 17  
|||  
|:|:|

Db 1 ATGVPIPY-APGE 12

## RESULT 7

B45115 peptidylprolyl isomerase (EC 5.2.1.8) FKBP51 - human (fragment)  
N:Alternative names: FK506-binding protein FKBP51; peptidylprolyl cis-trans isomerase FKBP  
C:Species: Homo sapiens (man)  
C:Date: 30-Apr-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
C:Accession: B45115  
R:Wiederricht, G.; Hung, S.; Chan, H.K.; Marcy, A.; Martin, M.; Calaycay, J.; Boulton, D  
J. Biol. Chem. 267, 21753-21760, 1992  
A:Title: Characterization of high molecular weight FK-506 binding activities reveals a n  
A:Reference number: A45115; MUID:93016131; PMID:1363226  
A:Accession: B45115  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-15 <WIE>  
A:Cross-references: UNIPROT:Q9UDK1; UNIPARC:UPI0000035473  
A:Experimental source: JURKAT cells  
A:Note: sequence extracted from NCBI backbone (NCBI:P116748)  
C:Keywords: cis-trans-isomerase; cyclosporin A binding

Query Match 23.7%; Score 23; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 1.5e+03;

Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 6 ATNIPFYTAP 15  
|||  
|:|:|

Db 1 ATESIAVYLP 10

## RESULT 8

S20322 gluten - wheat  
C:Species: Triticum aestivum (common wheat)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004



C/Accession: S20322  
 R/Fukudome, S.; Yoshikawa, M.  
 FEBS Lett. 296, 107-111, 1992  
 A/Title: Opioid peptides derived from wheat gluten: their isolation and characterization  
 C/Date: 05-Aug-1994 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 C/Accession: PN0170  
 R/Fukaya, N.; Chow, L.P.; Sugitara, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.  
 submitted to JIPID, May 1994  
 A/Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich  
 A/Reference number: PN0160  
 A/Accession: PN0170  
 A/Molecule type: protein  
 A/Residues: 1-12 <FUK>  
 A/Cross-references: UNIPROT:Q7M4Z9; UNIPARC:UPI000017B3F6  
 A/Experimental source: strain M-1-1  
 C/Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 22.7%; Score 22; DB 2; Length 12;  
 Best Local Similarity 66.7%; Pred. No. 1.7e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 12 YTAGK 17  
 DB 6 YVDGK 11

RESULT 10  
 S01904  
 H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Arabidopsis thaliana chloro  
 C/Species: chloroplast Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 09-Jul-2004  
 C/Accession: S01904  
 R/Chen, H.C.; Wintz, H.; Weill, J.H.; Pillay, D.T.N.  
 Nucleic Acids Res. 16, 10372, 1988  
 A/Title: Nucleotide sequence of chloroplast CFI-ATPase epsilon-subunit and elongator tRNA  
 C/Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 09-Jul-2004  
 A/Reference number: S01903; MUID:89057486; PMID:2904134  
 A/Accession: S01904  
 R/Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JIPID, October 1994  
 A/Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich  
 A/Reference number: PA0051  
 A/Accession: PA0099  
 A/Molecule type: protein  
 A/Residues: 1-15 <CHO>  
 A/Cross-references: UNIPROT:Q7M4Y7; UNIPARC:UPI000017B405  
 A/Experimental source: strain M-1-1  
 C/Keywords: ATP biosynthesis; chloroplast; hydrolase; thylakoid

Query Match 22.7%; Score 22; DB 2; Length 13;  
 Best Local Similarity 80.0%; Pred. No. 1.9e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 KATNI 9  
 DB 1 KATNL 5

RESULT 11  
 PA0056  
 Protein QP200002 - fungus (Fusarium sporotrichioides) (fragment)  
 C/Species: Fusarium sporotrichioides  
 C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Mar-2001  
 C/Accession: PA0056  
 R/Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JIPID, October 1994  
 A/Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich  
 A/Reference number: PA0051  
 A/Accession: PA0056  
 A/Molecule type: protein  
 A/Residues: 1-15 <CHO>  
 A/Cross-references: UNIPARC:UPI000017B408

Query Match 22.7%; Score 22; DB 2; Length 15;  
 Best Local Similarity 80.0%; Pred. No. 2.2e+03;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 ATNIF 10  
 DB 11 ATNIF 15

RESULT 12  
 PA0087  
 Cytochrome c2 - fungus (Fusarium sporotrichioides) (fragment)  
 C/Species: Fusarium sporotrichioides  
 C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C/Accession: PA0087  
 R/Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JIPID, October 1994  
 A/Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich  
 A/Reference number: PA0051  
 A/Accession: PA0087  
 A/Molecule type: protein  
 A/Residues: 1-15 <CHO>  
 A/Cross-references: UNIPROT:Q7M4Z7; UNIPARC:UPI000017B3F8  
 A/Experimental source: strain M-1-1  
 C/Keywords: electron transfer; heme; photosynthesis

Query Match 22.7%; Score 22; DB 2; Length 15;  
 Best Local Similarity 44.4%; Pred. No. 2.2e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 2 DGKATNIF 10  
 DB 4 DKKGNLIF 12

RESULT 13  
 PA0099  
 phenolic variation protein - fungus (Fusarium sporotrichioides) (fragment)  
 C/Species: Fusarium sporotrichioides  
 C/Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C/Accession: PA0099  
 R/Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
 submitted to JIPID, October 1994  
 A/Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich  
 A/Reference number: PA0051  
 A/Accession: PA0099  
 A/Molecule type: protein  
 A/Residues: 1-15 <CHO>  
 A/Cross-references: UNIPROT:Q7M4Y7; UNIPARC:UPI000017B405

Query Match 22.7%; Score 22; DB 2; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 2.2e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 10 FPYAPG 16  
 DB 7 FKYSASG 13

## RESULT 14

A28144  
 ribosomal protein S27a - bovine (fragment)  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 28-Aug-1989 #sequence\_revision 28-Aug-1989 #text\_change 09-Jul-2004  
 C/Accession: A28144  
 R/Redman, K.L.; Rechsteiner, M.  
 J. Biol. Chem. 263, 4926-4931, 1988  
 A/Title: Extended reading frame of a ubiquitin gene encodes a stable, conserved, basic P  
 A/Reference number: A28144; MUID:88169619; PMID:2832412  
 A/Accession: A28144  
 A/Molecule type: protein  
 A/Residues: 1-16 <RED>  
 A/Cross-references: UNIPROT:O97577; UNIPARC:UPI0000177161  
 C/Superfamily: ubiquitin / rat ribosomal protein S27a; ribosomal protein S27a homology;  
 C/Keywords: protein biosynthesis

## Query Match

Best Local Similarity 22.7%; Score 22; DB 2; Length 16;  
 Pred. No. 2.4e+03;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 YTPPK 17

Db 9 YTPPK 14

## RESULT 15

C84063  
 hypochemical protein BH3307 (imported) - Bacillus halodurans (strain C-125)  
 C/Species: Bacillus halodurans  
 C/Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 09-Jul-2004  
 C/Accession: C84063  
 R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
 A/Reference number: A83650; MUID:20512582; PMID:11058132  
 A/Accession: C84063  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-17 <STO>  
 A/Cross-references: UNIPROT:Q9K7Q4; UNIPARC:UPI00000C4168; GB:AP001518; GB:BA000004; NID  
 A/Experimental source: strain C-125  
 C/Genetics:  
 A/Gene: BH3307

## Query Match

Best Local Similarity 22.7%; Score 22; DB 2; Length 17;  
 Pred. No. 2.6e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DGQKATN 8

Db 10 DNKKQTN 16

Search completed: May 30, 2006, 15:08:21  
 Job time : 12 secs

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 30, 2006, 15:01:11 ; Search time 66.6667 Seconds  
(without alignments)  
242.480 Million cell updates/sec

Title: US-10-758-165a-10  
Perfect score: 97  
Sequence: 1 VDGOKATNIPFYTAPGKQ 18

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 12648

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 7.2: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	35.1	17	2	046473_FELCA
2	32	33.0	8	2	Q70Y88_9LAMI
3	28.5	29.4	18	2	Q9TWL4_LUCCU
4	27.5	28.4	16	2	Q8L1Y7_PLEBO
5	27	27.8	18	2	Q7M4W6_FLEAVE
6	26	26.8	15	2	Q7S007_NEUCR
7	26	26.8	18	2	Q7M198_STRFR
8	25	25.8	15	1	CPM16_LYCES
9	25	25.8	15	2	Q9UR63_EMENT
10	25	25.8	16	2	Q3ZEV4_9CHAR
11	24	24.7	14	2	Q714T5_9CRYP
12	24	24.7	16	2	Q7TPH9_PROSU
13	24	24.7	16	2	Q3ZEY6_9CHAR
14	24	24.7	17	2	Q65Y26_HORSE
15	24	24.7	18	2	Q3TW38_MOUSE
16	23	23.7	10	2	Q9Z1B1_CLODI
17	23	23.7	12	2	Q7M2G3_VICFA
18	23	23.7	14	1	CPW27_TOBAC
19	23	23.7	14	2	P78359_HUMAN
20	23	23.7	15	2	Q5D4R7_9CYAN
21	22	23.7	16	2	Q8L1Y8_9CYAN
22	23	23.7	16	2	Q89560_HHV8
23	23	23.7	17	2	Q9TWB9_ACACA
24	23	23.7	17	2	Q9PRU8_CHICK
25	23	23.7	18	2	Q7M1G0_WHEAT
26	22	22.7	8	2	Q59AB6_HUMAN
27	22	22.7	10	2	Q71VN2_MOUSE
28	22	22.7	10	2	Q9QVE9_9MURI
29	22	22.7	11	1	PVK1_PERYR
30	22	22.7	12	2	Q7M4Z6_FUSSP
31	22	22.7	14	2	Q70Y94_9LAMI

32	22	22.7	15	2	Q7M4V7_FUSGP	Q7M4V7_fusarium sp
33	22	22.7	15	2	Q7M4Z7_FUSSP	Q7M4Z7_fusarium sp
34	22	22.7	15	2	Q9TRB5_BOVIN	Q9TRB5_bos taurus
35	22	22.7	15	2	Q9TRB8_PIG	Q9TRB8_sus scrofa
36	22	22.7	16	2	Q70Y93_9LAMI	Q70Y93_platostoma
37	22	22.7	17	2	Q9K7Q4_BACDH	Q9K7Q4_bacillus ha
38	22	22.7	18	2	Q7M4Q7_HUMAN	Q7M4Q7_homo sapien
39	22	22.7	18	2	Q9TWL5_LUCCU	Q9TWL5_lucilia cup
40	22	22.7	18	2	Q9TRB6_PIG	Q9TRB6_sus scrofa
41	22	22.7	18	2	Q3ZSL3_HORVU	Q3ZSL3_hordeum vul
42	22	22.7	18	2	Q70Y99_9LAMI	Q70Y99_bacillus p
43	21.5	22.2	17	1	COG2_CARMA	P81609_carcinus ma
44	21	21.6	9	2	Q30750_BRWAM	Q30750_erwinia amy
45	21	21.6	9	2	Q65711_BEV	Q65711_berne virus

## ALIGNMENTS

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RESULT 1
ID 046473_FELCA PRELIMINARY; PRT; 17 AA.
AC 046473;
DT 01-JUN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JUN-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Lactase dehydrogenase A (Fragment).
GN Name=LDHA;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=domesticus;
RX MEDLINE=97141918; PubMed=8988168;
RA Lyons L.A., Laughlin T.F., Copeland N.G., Jenkins N.A., Womack J.E.,
RA O'Brien S.J.;
RT "Comparative anchor tagged sequences (CATS) for integrative mapping of
RT mammalian genomes.";
RL Nat. Genet. 15:47-56(1997).
CC -----
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CC -----
DR EMBL; AF012095; AAC00072.2; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 17
FT SEQUENCE 17 AA; 2018 MW; E47943B2E187C1FC CRC64;
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Best Local Similarity 46.2%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Oy 3 GOKATNIPFYTAP 15
Db 3 GORVNIFKFLIP 15
RESULT 2
ID 070Y88_9LAMI PRELIMINARY; PRT; 8 AA.
AC 070Y88;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Ribosomal protein (Fragment).
GN Name=tps16;
OS Platostoma fimbriatum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
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OC asterids; lamids; Lamiaceae; Nepetoideae; Ocimeae;  
OC Platanoma.  
OX NCBI\_TaxID=204168;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;  
RA Paton A., Springate D.A., Sude S., Otiemo D., Grayer R., Harley M.M.,  
Wills F., Simons M.S.J., Powell M.P., Savolainen V.;  
RT "Phylogeny and evolution of basils and allies (Ocimeae, Labiales)  
based on three plastid DNA regions";  
RL Mol. Phylogenet. Evol. 31:277-299(2004).  
CC -----  
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CC -----  
DR EMBL: AJ505368; CAD45489.1; -; Genomic DNA.  
DR GO: GO:0003735; F:structural constituent of ribosome, IEA.  
KM Ribosomal protein.  
FT NON\_TER 1 8  
FT NON\_TER 1 8  
SQ SEQUENCE 8 AA; 789 MW; 86786772D1BA4772 CRC64;  
  
Query Match 33.0%; Score 32; DB 2; Length 8;  
Best Local Similarity 83.3%; Pred. No. 2.8e+06;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
OY 11 PYTAPG 16  
Db 2 PYTVP 7  
  
RESULT 3  
O9TWM4 LUCCU PRELIMINARY; PRT; 18 AA.  
AC O9TWM4;  
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
DT 07-FEB-2006, entry version 1.  
DE 25 kDa chymotrypsin-like enzyme (Fragment).  
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pelegridae;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
OC Calliphoridae; Lucilia.  
OX NCBI\_TaxID=7375;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=95219141; PubMed=7704304;  
RA Casu R.E., Pearson R.D., Jarney J.M., Cadogan L.C., Ridding G.A.,  
Tallam R.L.;  
RT "Excretory/secretory chymotrypsin from Lucilia cuprina: purification,  
enzymatic specificity and amino acid sequence deduced from mRNA";  
RL Insect Mol. Biol. 3:201-211(1994).  
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CC -----  
SQ SEQUENCE 18 AA; 1922 MW; 352EB0729B126B11 CRC64;  
  
Query Match 29.4%; Score 28.5; DB 2; Length 18;  
Best Local Similarity 58.3%; Pred. No. 2.3e+03;  
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;  
  
OY 2 DQQRAT-NIPFY 12  
Db 3 NGQEAIVGQFPY 14  
  
RESULT 4  
O8LIY7 PLEBO PRELIMINARY; PRT; 16 AA.  
AC O8LIY7;  
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2002, sequence version 1.

DT 07-FEB-2006, entry version 7.  
DE Proteolysis-inducing tag (Fragment).  
OS Plectonema boryanum.  
OC Bacteria; Cyanobacteria; Oscillatoriales; Lepidymnobia.  
OX NCBI\_TaxID=1184;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX STRAIN=UTEX 485;  
RT MEDLINE=21970088; PubMed=11972342; DOI=10.1093/nar/30.9.2025;  
RA Williams K.P.;  
RT "Descent of a split RNA";  
RL Nucleic Acids Res. 30:2025-2030(2002).  
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CC -----  
DR EMBL: AY082652; AAM03311.1; -; Genomic DNA.  
FT NON\_TER 1 1  
FT NON\_TER 1 1  
SQ SEQUENCE 16 AA; 1640 MW; 60FE5985B9B00982 CRC64;  
  
Query Match 28.4%; Score 27.5; DB 2; Length 16;  
Best Local Similarity 53.8%; Pred. No. 3.1e+03;  
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;  
  
OY 6 ATNIFPY---TAP 15  
Db 1 ANNIVPFARKTAP 13  
  
RESULT 5  
Q7M4W6 FLAVE PRELIMINARY; PRT; 18 AA.  
AC Q7M4W6;  
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.  
DT 15-DEC-2003, sequence version 1.  
DE 07-FEB-2006, entry version 6.  
DE Protein P11 (Fragment).  
OS Flammulina velutipes.  
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
OC Agaricales; Tricholomataceae; Flammulina.  
OX NCBI\_TaxID=38945;  
RN [1]  
RP PROTEIN SEQUENCE.  
RA Sakamoto Y., Ando A., Tamai Y., Miura K.;  
RL Submitted (NOV-1999) to the PIR data bank.  
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DR PIR: A59137; A59137.  
FT NON\_TER 1 1  
FT NON\_TER 1 1  
SQ SEQUENCE 18 AA; 1956 MW; FB0434B0AF005AEC CRC64;  
  
Query Match 27.8%; Score 27; DB 2; Length 18;  
Best Local Similarity 80.0%; Pred. No. 4.2e+03;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
OY 11 PYTAP 15  
Db 2 PYTSP 6  
  
RESULT 6  
Q7S007 NEUCR PRELIMINARY; PRT; 15 AA.  
AC Q7S007;  
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.  
DT 15-DEC-2003, sequence version 1.  
DE 07-FEB-2006, entry version 8.  
DE Predicted protein.  
GN ORFNames=NCU09752.1;  
OS Neurospora crassa.

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OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
[1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
RA Elkins T., Engle R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A.,
RA Werner-Washburne M., Selitrenikoff C.P., Kinsey J.A., Braun E.L.,
RA Zelter A., Schulte U., Kothe G.O., Uedd G., Mewes H.-W., Staben C.,
RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA Stange-Thomann N., Barrett R., Gierke S., Kamal M., Kamyssele M.,
RA Mauceli E., Bielke C., Rudd S., Fishman D., Krysosova S.,
RA Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S., Cogoni C.,
RA Marino G., Catchside D.E.A., Li W., Pratt R.J., Omani S.A.,
RA Desouza C.P.C., Glas N.L., Orbach M.J., Berglund J.A., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J.C., Radford A., Aramayo R.,
RA Navig D.O., Alex L.A., Mannheim G., Ebole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.W.;
RT "The genome sequence of the filamentous fungus Neurospora crassa.";
RL Nature 422:859-868(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AABX01000580; EAA28619.1; -; Genomic DNA.
SQ SEQUENCE 15 AA; 1832 MW; 012D0180A8C7089D CRC64;

Query March 26.8%; Score 26; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 5.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 NIPPT 13
| | | |
Db 2 NVFPT 7

RESULT 7
Q7M198 STRFR PRELIMINARY; PRT; 18 AA.
ID Q7M198 STRFR
AC Q7M198
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE 24k serine proteinase (EC 3.4.21.-) (Fragment).
OS Streptomyces fradiae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1906;
[1]
RN PROTEIN SEQUENCE.
RX MEDLINE=92155439; PubMed=1786859; DOI=10.1016/0020-711X(92)90133-8;
RA Silha U., Woltz S.A., Lad P.J.;
RT "Two new extracellular serine proteases from Streptomyces fradiae.";
RL Int. J. Biochem. 23:979-984(1991).
CC -----
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CC -----
DR PIR; A61577; A61577.
CC -----
FT NON_TER 1
FT TER 18
SQ SEQUENCE 18 AA; 2004 MW; 6D6DA167845934A5 CRC64;

Query March 26.8%; Score 26; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 6.2e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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QY 1 VDGOXATNIPFY 12
| | | | |
Db 2 VGTTRAQGEFPW 13

RESULT 8
CWP16_LYCES STANDARD; PRT; 15 AA.
ID CWP16_LYCES
AC P80812;
DT 25-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE 40 kDa cell wall protein (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Ascomycota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
OX NCBI_TaxID=4081;
[1]
RN PROTEIN SEQUENCE, AND SUBCELLULAR LOCATION.
RP MEDLINE=9733671; PubMed=918482; DOI=10.1074/jbc.272.25.15841;
RX Robertson D., Mitchell G.P., Gilroy J.G., Gerrish C., Bolwell G.P.,
RA Slabas A.R.;
RT "Differential extraction and protein sequencing reveals major
RT differences in patterns of primary cell wall proteins from plants.";
RL J. Biol. Chem. 272:15841-15846(1997).
CC -!- SUBCELLULAR LOCATION: Cell wall.
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
KW Cell wall; Direct protein sequencing.
FT CHAIN 1
FT 1 >15
FT /FTID=PRO_0000079677.
SQ SEQUENCE 15 AA; 1705 MW; 1F3285C82CA77BE CRC64;

Query March 25.8%; Score 25; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 FPPT 13
| | | | |
Db 6 FPPT 9

RESULT 9
O9UR63_EMENT PRELIMINARY; PRT; 15 AA.
ID O9UR63_EMENT
AC O9UR63;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Beta-D-FRUCTOFURANOSIDE FRUCTOHYDROLASE 60 kDa high molecular weight
DE isoform (EC 3.2.1.26) (Fragment).
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
[1]
RN PROTEIN SEQUENCE.
RP MEDLINE=96409246; PubMed=8814228; DOI=10.1016/0167-4838(96)00073-8;
RX Chen J.S., Saxton J., Hemming F.W., Peberdy J.F.;
RT "Purification and partial characterization of the high and low
RT molecular weight form (S- and F-form) of invertase secreted by
RT Aspergillus nidulans.";
RL Biochim. Biophys. Acta 1296:207-218(1996).
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
DR GO; GO:0004564; F-beta-fructofuranosidase activity; IEA.

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SEQ SEQUENCE 15 AA; 1588 MW; 2C992B42211366BB CRC64;

Query Match 25.8%; Score 25; DB 2; Length 15;

Best Local Similarity 80.0%; Pred. No. 7.6e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 PYTAP 15

DB 10 PYTAP 14

RESULT 10

O3ZEV4\_9CHAR PRELIMINARY; PRT; 16 AA.

AC O3ZEV4\_7 PRELIMINARY; PRT; 16 AA.

DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.

DT 27-SEP-2005, sequence version 1.

DT 07-FEB-2006, entry version 3.

DE ATP synthase F0 subunit 8 (Fragment).

GN Name=ATP8;

OS Tringa totanus.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Charadriiformes; Scolopacidae; Tringa.

NCBI\_TaxID=171271;

[1]

NP NUCLEOTIDE SEQUENCE.

RA Pereira S.L., Baker A.J.;

RT "Multiple gene evidence for parallel evolution and retention of

RT Scolopacidae)." ;

RL Condor 107:514-526 (2005).

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CC EMBL; AY894271; AAX94014.1; -; Genomic DNA.

DR GO; GO:0005739; C:mitochondrion; IEA.

KW Mitochondrion.

FT NON\_TER 1

SEQ SEQUENCE 16 AA; 1965 MW; 75D680373ACCF82D CRC64;

Query Match 25.8%; Score 25; DB 2; Length 16;

Best Local Similarity 55.6%; Pred. No. 8.2e+03;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 7 TNIFPYTAP 15

DB 6 TKIRPTWTP 14

RESULT 11

O71AT5\_9CRYP PRELIMINARY; PRT; 14 AA.

AC O71AT5;

DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.

DT 05-JUL-2004, sequence version 1.

DT 07-FEB-2006, entry version 7.

DE tRNA proleucyls tag (Fragment).

GN Name=sara;

OS Rhodomonas salina.

OC Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.

NCBI\_TaxID=52970;

[1]

NP NUCLEOTIDE SEQUENCE.

RA STRAIN=CCMP1319;

RA PubMed=14681369; DOI=10.1093/nar/gkh102;

RA Gueneau de Novoa P., Williams K.P.;

RT "The tRNA website: reductive evolution of tRNA in plastids and other

RT endosymbionts." ;

RL Nucleic Acids Res. 32:D104-D108 (2004).

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DR EMBL; AF550355; AAQ12671.1; -; Genomic DNA.

FT NON\_TER 1

SEQ SEQUENCE 14 AA; 1528 MW; D995F9B3698210B9 CRC64;

Query Match 24.7%; Score 24; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 1e+04;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 ATNIFPYT 13

DB 1 ANNIIVPFS 8

RESULT 12

O7TPH9\_PHOSU PRELIMINARY; PRT; 16 AA.

AC O7TPH9;

DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.

DT 01-OCT-2003, sequence version 1.

DT 07-FEB-2006, entry version 7.

DE Per2 protein (Fragment).

GN Name=Per2;

OS Phodopus sungorus (Striped hairy-footed hamster) (Djunganian hamster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridea; Cricetidae; Cricetinae; Phodopus.

NCBI\_TaxID=10044;

[1]

NP NUCLEOTIDE SEQUENCE.

RA Souza V., Semikhodskii A.G., London A.S.I.;

RT Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

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CC EMBL; AY316536; AAP87362.1; -; mRNA.

DR NON\_TER 1

SEQ SEQUENCE 16 AA; 1831 MW; 845CE49E44AE531 CRC64;

Query Match 24.7%; Score 24; DB 2; Length 16;

Best Local Similarity 50.0%; Pred. No. 1.2e+04;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 11 PYTAPKQ 18

DB 6 PLTSPRKE 13

RESULT 13

O3ZEV6\_9CHAR PRELIMINARY; PRT; 16 AA.

AC O3ZEV6;

DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.

DT 27-SEP-2005, sequence version 1.

DT 07-FEB-2006, entry version 3.

DE ATP synthase F0 subunit 8 (Fragment).

GN Name=ATP8;

OS Tringa flavipes.

OC Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Charadriiformes; Scolopacidae; Tringa.

NCBI\_TaxID=161739;

[1]

NP NUCLEOTIDE SEQUENCE.

RA Pereira S.L., Baker A.J.;

RT "Multiple gene evidence for parallel evolution and retention of

RT Scolopacidae)." ;

RL Condor 107:514-526 (2005).

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 CC EMBL: AY894261; AAX93984.1; -; Genomic\_DNA.  
 DR GO: 0005739; C:mitochondrion; IEA.  
 KM Mitochondrion.  
 FT NON\_TER 1  
 SQ SEQUENCE 16 AA; 1893 MW; 6FF80272A4F1F82D CRC64;  
 Query Match 24.7%; Score 24; DB 2; Length 16;  
 Best Local Similarity 50.0%; Pred. No. 1.2e+04;  
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 Oy 6 ATNIPYAP 15  
 Db 5 ATKTPWTWP 14  
 RESULT 14  
 ID 065Y26 HORSE PRELIMINARY; PRT; 17 AA.  
 AC 065Y26;  
 DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.  
 DT 25-OCT-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 6.  
 DE Asparagine-linked glycosylation 8 homolog (Fragment).  
 GN Name=ALG8;  
 OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Hasegawa T., Sato F., Tozaki T., Hirota K.;  
 RT "Fine mapping of equine chromosomes corresponding to HSA11";  
 RL Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.  
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 CC EMBL: AB167785; BAD44704.1; -; Genomic\_DNA.  
 DR SNR: 065Y26; 1-72.  
 DR SNR: 065Y26; BAD44704.1; -; Genomic\_DNA.  
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 FT NON\_TER 17  
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 Query Match 24.7%; Score 24; DB 2; Length 17;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+04;  
 Matches 5; Conservative 3; Mismatches 0; Indels 2; Gaps 1;  
 Oy 8 NIFP-YTAP 15  
 Db 6 SLFPLFTAP 15  
 RESULT 15  
 ID 03TW38 MOUSE PRELIMINARY; PRT; 18 AA.  
 AC 03TW38;  
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.  
 DT 11-OCT-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 5.  
 DE Oseoclast-like cell cDNA, RIKEN full-length enriched library,  
 DE clone:1420034D23 product: RNA binding motif, single stranded  
 DE interacting protein 1, full insert sequence. (Fragment).  
 GN Name=Bme1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning";  
 RL Methods Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J;  
 RX PubMed=16141072; DOI=10.1126/science.1112014;  
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maida N.,  
 Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,  
 Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,  
 Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,  
 Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
 Bansal M., Baxter L., Belsel K.W., Bersano T., Bono H., Chaik A.M.,  
 Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
 Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
 di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,  
 Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
 Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
 Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
 Hill D., Hummelich L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
 Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,  
 Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
 Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
 Linu S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
 Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
 Mottagui-Tabar S., Mulder N., Nakano N., Nakanchi H., Ng P.,  
 Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
 Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,  
 Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
 Roest B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
 Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,  
 Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
 Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,  
 Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
 Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K.,  
 Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
 Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
 Wahlestedt C., Watnick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
 Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arikawa T.,  
 Iida Y., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashita N.,  
 Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Ninomiya N.,  
 Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,  
 Tagami M., Waki K., Watanuki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
 Hayashizaki Y.;  
 RT "The transcriptional landscape of the mammalian genome";  
 RL Science 309:1559-1563(2005).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J;  
 RX PubMed=16141073; DOI=10.1126/science.1112009;  
 RG RIKEN Genome Exploration Research Group, and Genome Science Group  
 (Genome Network Core Team) and the FANTOM Consortium;  
 RT "Antisense Transcription in the Mammalian Transcriptome";  
 RL Science 309:1564-1566(2005).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J;  
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
 Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 Schriml L.M., Kanapin A., Matsumura H., Batalov S., Beisel K.W.,  
 Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,  
 Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 Maglott D.R., Matsuda L., Marchionni L., McKenzie L., Miki H.,  
 Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Wanabe Y., Wells C.,  
RA Wilming L.G., Wyshaw-Borje A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavalon M., Zhu Y., Zimmer A., Carinci P., Hayatsu N.,  
RA Hironaka-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Maki K., Kawai J., Aizawa K., Atakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imocant K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yaunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).  
[5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Atakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schirni L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Guenrich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombere P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wyshaw-Borje A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
[6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carinci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RT prepare full-length cDNA libraries for rapid discovery of new genes."  
RL Genome Res. 10:1617-1630(2000).  
[7]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carinci P.,  
RA Kono H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,  
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RT sequencing pipeline with 384 multicapillary sequencer."  
RL Genome Res. 10:1757-1771(2000).  
[8]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J;  
RA Atakawa T., Carinci P., Fukuda S., Hashizume W., Hayashida K.,  
RA Hori F., Iida J., Imamura K., Imocant K., Itoh M., Kanagawa S.,  
RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Ninomiya N.,  
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,  
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Wataniki A.,  
RA Muramatsu M., Hayashizaki Y.;  
RT Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

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CC -----  
DR EMBL: AK159851; BAB35428.1; -; mRNA.  
DR MGI: MGI:1861774; Rbm31.  
DR GO: GO:0005634; C:nucleus; RCA.  
DR GO: GO:0003690; C:nucleus; RCA.  
DR GO: GO:0003723; F:RNA binding; RCA.  
DR GO: GO:0003657; F:single-stranded DNA binding; RCA.  
DR GO: GO:0006260; P:DNA replication; RCA.  
FT NON TER 1 1  
SQ SEQUENCE 18 AA; 2003 MW; 82F8A5FD94E8A14 CRC64;  
Query Match 24.7%; Score 24; DB 2; Length 18;  
Best Local Similarity 80.0%; Pred. No. 1.4e+04;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
OY 11 PYTP 15  
DB 11 PYTP 15  
Search completed: May 30, 2006, 15:07:41  
Job time : 69.6667 secs



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OM protein - protein search, using sw model

Run on: May 30, 2006, 14:59:31 ; Search time 61.6667 Seconds  
(without alignments)  
133.458 Million cell updates/sec

Title: US-10-758-165A-10  
Perfect score: 97  
Sequence: 1 VDCQKATNIPPTAPGKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 902922

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	18	ADRI0610	Adt10610 Cat IGE e
2	87	89.7	18	ADRI0609	Adt10609 Dog IGE e
3	55	56.7	18	ADRI0612	Adt10612 Sheep IGE
4	37	38.1	15	ADCS6890	Adc56890 Peptide f
5	35	36.1	18	ADRI0611	Adt10611 Horse IGE
6	34	35.1	15	ADCS6890	Adc64569 Horse imm
7	33.5	34.5	15	ADJ38597	Adj38597 HSV-4 G1Y
8	32.5	33.5	15	ADJ38596	Adj38596 HSV-4 G1Y
9	32.5	33.5	15	ADW78189	Adw78189 Human met
10	32	33.0	9	AAU76520	Aau76520 Anti-Inte
11	32	33.0	9	AAE15818	Aae15818 Human mab
12	32	33.0	9	AEF76312	Aef76312 Prostate
13	32	33.0	11	ADT40399	Adt40399 hSARS vir
14	32	33.0	11	ADST79816	Adst79816 SARS viru
15	32	33.0	11	ADT37929	Adt37929 hSARS vir
16	32	33.0	15	AAV65747	Aav65747 Breast ca
17	32	33.0	15	ABU78631	Abu78631 Novel pro
18	32	33.0	15	ABU78640	Abu78640 Novel pro
19	32	33.0	15	ADN64911	Adn64911 HLA bindi
20	31	32.0	11	AAE02349	Aae02349 Caenorhab
21	31	32.0	12	AAK90344	Aak90344 Macrophab
22	31	32.0	13	ADBJ37003	Adbj37003 Stainless
23	31	32.0	14	AAV31329	Aav31329 B. subtil

24	31	32.0	15	8	ADN64927	Adn64927 HLA bindi
25	31	32.0	15	9	ADM77997	Adm77997 Human can
26	30	30.9	9	6	ABU19961	Abu19961 MHC bindi
27	30	30.9	9	7	ADD94584	Add94584 Human SIM
28	30	30.9	10	7	ADD94544	Add94544 Human SIM
29	30	30.9	11	9	ABE17405	Abe17405 Type II p
30	30	30.9	12	2	AAK49911	Aak49911 Glutamin
31	30	30.9	13	2	AAK49912	Aak49912 Glutamin
32	30	30.9	13	2	AAK49913	Aak49913 Glutamin
33	30	30.9	14	2	AAK49914	Aak49914 Glutamin
34	30	30.9	14	3	AAK39162	Aak39162 Human sec
35	30	30.9	14	3	AAK39163	Aak39163 Human sec
36	30	30.9	15	2	AAK65210	Aak65210 Murine st
37	30	30.9	15	9	ADU70842	Adu70842 Human hep
38	30	30.9	16	2	AAK53562	Aak53562 Birch pol
39	30	30.9	16	8	ADQ90450	Adq90450 RANTES re
40	30	30.9	17	2	AAK95159	Aak95159 bcl-x(L)/
41	30	30.9	18	9	ADV22975	Adv22975 HCV H77.1
42	29	29.9	9	2	AAW24775	Aaw24775 Human imm
43	29	29.9	9	2	AAW80144	Aaw80144 Light cha
44	29	29.9	9	2	AAW80142	Aaw80142 Light cha
45	29	29.9	9	2	AAV40427	Aav40427 Amino aci

## ALIGNMENTS

RESULT 1  
ADRI0610  
ID ADRI0610 standard; peptide: 18 AA.  
XX  
AC ADRI0610;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Cat IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 10.  
XX  
KM Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
cat.  
XX  
OS Fells catus.  
XX  
WO2004065936-A2.  
XX  
PD 05-AUG-2004.  
XX  
PF 15-JAN-2004; 2004WO-US003566.  
XX  
PR 16-JAN-2003; 2003US-0440472P.  
XX  
PA (UYNC-) UNIV NORTH CAROLINA STATE.  
XX  
PI Hammerberg B;  
XX  
DR WPI; 2004-593545/57.  
XX  
PT Novel antibody that specifically binds to mammalian IGE epitope, useful  
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
PT or treating asthma or anaphylactic shock.  
XX  
PS Example 6; Page 9; 14pp; English.  
XX  
XX The present invention relates to a novel monoclonal antibody (I) that  
XX specifically binds to a mammalian IGE epitope, where the epitope is  
XX between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
XX (I) is useful for testing an allergen reactivity of an IGE sample. The  
XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
XX and corn allergens. The sample is a biological sample collected from a  
XX dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
XX antibodies recognise epitopes on canine IGE corresponding to amino acid  
XX residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the

CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
CC either pig or human epsilon-chains of IGE. The present sequence is the  
CC cat IGE 3.76 recognition site.  
XX

SO Sequence 18 AA;

Query Match 100.0%; Score 97; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 5,7e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDGGKATNIFPYTAPGKQ 18  
Db 1 VDGGKATNIFPYTAPGKQ 18

RESULT 2

ADRI0609  
ID ADRI0609 standard; peptide; 18 AA.

XX AC ADRI0609;

XX DT 21-OCT-2004 (first entry)

XX DE Dog IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 9.

XX KW Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;

XX KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.

XX OS Canis familiaris.

XX PN WO2004065936-A2.

XX PD 05-AUG-2004.

XX PF 15-JAN-2004; 2004WO-US003566.

XX PR 16-JAN-2003; 2003US-0440472P.

XX PA (UYN-) UNIV NORTH CAROLINA STATE.

XX PI Hammerberg B;

XX DR WPI; 2004-593545/57.

XX PT Novel antibody that specifically binds to mammalian IGE epitope, useful  
XX for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
XX or treating asthma or anaphylactic shock.

XX PS Example 6; Page 9; 14pp; English.

XX CC The present invention relates to a novel monoclonal antibody (I) that  
XX specifically binds to a mammalian IGE epitope, where the epitope is  
XX between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
XX (I) is useful for testing an allergen reactivity of an IGE sample. The  
XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
XX and corn allergens. The sample is a biological sample collected from a  
XX dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
XX antibodies recognise epitopes on canine IGE corresponding to amino acid  
XX residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
XX canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
XX cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
XX 3.76 were observed to have good cross-reactivity with the epsilon-chain  
XX of IGE from cat and horse, but did not exhibit cross-reactivity with  
XX either pig or human epsilon-chains of IGE.

SO Sequence 18 AA;

Query Match 89.7%; Score 87; DB 8; Length 18;  
Best Local Similarity 100.0%; Pred. No. 2,7e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDGGKATNIFPYTAPG 16  
Db 1 VDGGKATNIFPYTAPG 16

RESULT 3

ADRI0612  
ID ADRI0612 standard; peptide; 18 AA.

XX AC ADRI0612;

XX DT 21-OCT-2004 (first entry)

XX DE Sheep IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 12.

XX KW Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;

XX KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;

XX OS Ovis aries.

XX PN WO2004065936-A2.

XX PD 05-AUG-2004.

XX PF 15-JAN-2004; 2004WO-US003566.

XX PR 16-JAN-2003; 2003US-0440472P.

XX PA (UYN-) UNIV NORTH CAROLINA STATE.

XX PI Hammerberg B;

XX DR WPI; 2004-593545/57.

XX PT Novel antibody that specifically binds to mammalian IGE epitope, useful  
XX for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
XX or treating asthma or anaphylactic shock.

XX PS Example 6; Page 9; 14pp; English.

XX CC The present invention relates to a novel monoclonal antibody (I) that  
XX specifically binds to a mammalian IGE epitope, where the epitope is  
XX between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
XX (I) is useful for testing an allergen reactivity of an IGE sample. The  
XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
XX and corn allergens. The sample is a biological sample collected from a  
XX dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
XX antibodies recognise epitopes on canine IGE corresponding to amino acid  
XX residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
XX canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
XX cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
XX 3.76 were observed to have good cross-reactivity with the epsilon-chain  
XX of IGE from cat and horse, but did not exhibit cross-reactivity with  
XX either pig or human epsilon-chains of IGE. The present sequence is the  
XX sheep IGE 3.76 recognition site.

SO Sequence 18 AA;

Query Match 56.7%; Score 55; DB 8; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.067;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 VDGGKATNIFPYTAP 15  
Db 1 VDGGEDRNLFPSYAP 15

RESULT 4  
ADCS6890

```

ID ADC56890 standard; peptide: 15 AA.
XX
AC ADC56890;
XX
DT 18-DEC-2003 (first entry)
XX
DE Peptide fragment Seq ID7 related to human protein 36-41.
XX
KW human; protein 36-41; arrhythmia; asthma; dementia.
XX
OS Homo sapiens.
XX
PN CN1382718-A.
XX
PD 04-DEC-2002.
XX
PF 26-APR-2001; 2001CN-00112751.
XX
PR 26-APR-2001; 2001CN-00112751.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2003-269480/27.
XX
PT New human macroprotein-36-41, encoding polynucleotide, antagonist and
PT recombinant production, useful for treating dementia, arrhythmia, asthma
PT and digestive ulcers.
XX
PS Example 6; SEQ ID NO 7; 33pp; Chinese.
XX
CC This invention relates to a novel protein, human protein 36-41, and the
CC DNA sequence encoding it. The protein of the invention may be useful for
CC the treatment of diseases such as arrhythmia, asthma and dementia. The
CC present sequence is the amino acid sequence of a peptide fragment of
CC human protein 36-41 which was used in the exemplification of the
CC invention.
XX
SQ Sequence 15 AA;

Query Match 38.1%; Score 37; DB 7; Length 15;
Best Local Similarity 40.0%; Pred. No. 59;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGGKATNIPPYTAP 15
   :|||:|:|:|
Db 1 MDGKMQPNSFPWQSP 15

RESULT 5
ADRI0611
ID ADRI0611 standard; peptide: 18 AA.
XX
AC ADRI0611;
XX
DT 21-OCT-2004 (first entry)
XX
DE Horse IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 11.
XX
KW Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
KW horse.
XX
OS Equus caballus.
XX
PN WO2004065936-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US003566.
XX
PR 16-JAN-2003; 2003US-0440472P.

```

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XX
PA (UNNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hammerberg B;
XX
DR WPI; 2004-593545/57.
XX
PT Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.
XX
PS Example 6; Page 9; 14pp; English.
XX
CC The present invention relates to a novel monoclonal antibody (I) that
CC specifically binds to a mammalian IGE epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC (I) is useful for testing an allergen reactivity of an IGE sample. The
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IGE corresponding to amino acid
CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IGE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IGE. The present sequence is the
CC horse IGE 3.76 recognition site.
XX
SQ Sequence 18 AA;

Query Match 36.1%; Score 35; DB 8; Length 18;
Best Local Similarity 44.4%; Pred. No. 1.6e+02;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 VDGGKATNIPPYTAPGKQ 18
   :|||:|:|:|
Db 1 IDGQRVDEQFPQHGVLVKQ 18

RESULT 6
ADC64569
ID ADC64569 standard; peptide: 15 AA.
XX
AC ADC64569;
XX
DT 18-DEC-2003 (first entry)
XX
DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide P5.
XX
KW Horse; immunoglobulin E; IGE; heavy chain; immunogen; allergy.
XX
OS Equus caballus.
XX
PN US2003087314-A1.
XX
PD 08-MAY-2003.
XX
PF 08-NOV-2001; 2001US-00052788.
XX
PR 08-NOV-2001; 2001US-00052788.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Gershwin LJ, Pettigrew HD, Kalina WV;
XX
DR WPI; 2003-765437/72.
XX
PT Immunogenic composition comprising an isolated equine immunoglobulin E
PT polypeptide that induces production of antibodies which specifically bind
PT to equine immunoglobulin E.
XX

```

PS Example 1; Page 8; 14pp; English.

XX The invention relates to an immunogenic composition comprising an  
CC isolated polypeptide having an amino acid sequence that is at least 80%  
CC identical to 6 (SI-56), 15 amino acid peptide sequences derived from  
CC equine immunoglobulin E (the composition induces production of an  
CC antibody that specifically binds to equine immunoglobulin (Ig)E, the six  
CC polypeptides are not explicitly identified in the specification. Also  
CC included are a composition comprising an antibody that specifically binds  
CC to a polypeptide at least 80% identical to (SI)-(56), an antibody that  
CC specifically binds to equine IgE made by the process of immunising an  
CC animal with a polypeptide at least 80% identical to (SI)-(56), making an  
CC antibody that specifically binds to equine IgE (involving immunising an  
CC animal with a composition further comprising an isolated polypeptide (the  
CC amino acid sequence of the polypeptide is at least 80% identical to (SI)-  
CC (56)), and collecting antiserum from the animal) and a kit for detection  
CC of equine IgE in a biological sample comprising the antibody and means  
CC for detecting specific binding of the antibody to equine IgE. The  
CC antibody is useful for detecting equine IgE protein in a biological  
CC sample (serum) which involves contacting the sample with the antibody,  
CC thus forming an antigen/antibody complex, and detecting the presence or  
CC absence of the antigen/antibody complex. The antibody and antigen are  
CC immobilised on a solid surface. The antibody is labelled such that the  
CC complex can be detected. The complex is detected using a second labelled  
CC antibody. The peptides are useful for generating antibodies specific for  
CC IgE which can serve as a diagnostic test for allergy. The present  
CC sequence is a Horse immunoglobulin E, IgE, heavy chain immunogenic  
CC peptide from the middle portion of the C2 region.

XX Sequence 15 AA;

Query Match 35.1%; Score 34; DB 7; Length 15;  
Best Local Similarity 54.5%; Pred. No. 1.9e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDGGKATNIFP 11  
: |||||  
Db 2 IDGQKVDEQFP 12

RESULT 7  
ADJ38597  
ID ADJ38597 standard; peptide; 15 AA.

XX ADJ38597;

AC ADJ38597;

XX 06-MAY-2004 (first entry)

DE HSV-4 Glycoprotein B late domain motif mutant peptide #1.

XX Virucide; HSV infection; antiviral; late domain motif; mutein; mutant.

XX Human herpesvirus 4.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 6 /note= "Wild-type residue replaced with Ala"

XX WO2004009027-A2.

XX 29-JAN-2004.

XX 21-JUL-2003; 2003WO-US022828.

XX 19-JUL-2002; 2002US-0397265P.

XX 19-JUL-2002; 2002US-0397477P.

XX 03-MAR-2003; 2003US-0451903P.

XX (MYRI-) MYRIAD GENETICS INC.

XX Morham S, Zavitz K, Hobden A;

XX WPI; 2004-123282/12.

DR Use of cells displaying herpes simplex virus (HSV) altered budding  
XX phenotype for the manufacture of a medicament for treating HSV infection.  
PT Example 13; Page 66; 74pp; English.

PS The present invention relates to cells displaying herpes simplex virus  
XX (HSV) altered budding phenotype which are useful for the manufacture of a  
CC medicament for treating HSV infection. The medicament further comprises  
CC an adjuvant capable of stimulating cellular immune response e.g. IL-2, IL-  
CC 4, IL-12, IL-18 or gamma-interferon. The cells are human cells and  
CC contain a nucleic acid encoding a mutant HSV protein or a nucleic acid  
CC encoding the polypeptide sufficient for virus-like particle assembly but  
CC devoid of late-domain motifs. The nucleic acid is within an HSV genome.  
CC The genome is devoid of late domain motifs capable of effecting viral  
CC budding. The composition also comprises a compound capable of interfering  
CC with the protein-protein interaction between a host cell protein capable  
CC of binding a late domain motif and a HSV protein containing a late domain  
CC motif. The composition further comprises another HSV protein or its  
CC immunogenic fragment, and/or a nucleic acid encoding the other HSV  
CC protein or the immunogenic fragment. The present sequence is a mutant HSV  
CC peptide, derived from the wild-type peptide ADJ38596, used to illustrate  
CC the invention.

XX Sequence 15 AA;

Query Match 34.5%; Score 33.5; DB 8; Length 15;  
Best Local Similarity 66.7%; Pred. No. 2.3e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 6 ATNIFPYTAPCK 17  
|||: |||||  
Db 1 ATTV-PATAPCK 11

RESULT 8  
ADJ38596  
ID ADJ38596 standard; peptide; 15 AA.

XX ADJ38596;

XX 06-MAY-2004 (first entry)

DE HSV-4 Glycoprotein B late domain motif wild-type peptide.

XX Virucide; HSV infection; antiviral; late domain motif.

XX Human herpesvirus 4.

OS WO2004009027-A2.

XX 29-JAN-2004.

XX 21-JUL-2003; 2003WO-US022828.

XX 19-JUL-2002; 2002US-0397265P.

XX 19-JUL-2002; 2002US-0397477P.

XX 03-MAR-2003; 2003US-0451903P.

XX (MYRI-) MYRIAD GENETICS INC.

XX Morham S, Zavitz K, Hobden A;

XX WPI; 2004-123282/12.

DR Use of cells displaying herpes simplex virus (HSV) altered budding  
XX phenotype for the manufacture of a medicament for treating HSV infection.  
PT Example 13; Page 66; 74pp; English.

XX Example 13; Page 66; 74pp; English.

CC The present invention relates to cells displaying herpes simplex virus  
CC (HSV) altered budding phenotype which are useful for the manufacture of a  
CC medicament for treating HSV infection. The medicament further comprises  
CC an adjuvant capable of stimulating cellular immune response e.g. IL-2, IL  
CC -4, IL-12, IL-18 or gamma-interferon. The cells are human cells and  
CC contain a nucleic acid encoding a mutant HSV protein or a nucleic acid  
CC encoding the polypeptide sufficient for virus-like particle assembly but  
CC devoid of late-domain motifs. The nucleic acid is within an HSV genome.  
CC The genome is devoid of late domain motifs capable of effecting viral  
CC budding. The composition also comprises a compound capable of interfering  
CC with the protein-protein interaction between a host cell protein capable  
CC of binding a late domain motif and a HSV protein containing a late domain  
CC motif. The composition further comprises another HSV protein or its  
CC immunogenic fragment, and/or a nucleic acid encoding the other HSV  
CC protein or the immunogenic fragment. The present sequence is a wild-type  
CC HSV peptide, from which mutant sequences (ADJ38597-ADJ38600) were  
CC generated for use in the invention.

XX Sequence 15 AA;

Query Match 33.5%; Score 32.5; DB 8; Length 15;

Best Local Similarity 66.7%; Pred. No. 3.4e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 6 ATNIFPYTPARK 17  
||| |||||  
DB 1 ATTV-PTTPARK 11

RESULT 9

ADW78189

ID ADW78189 standard; peptide; 15 AA.

XX AC ADW78189;

DT 07-APR-2005 (first entry)

XX DE Human metabolic therapy target peptide PACT.

XX DEF domain; MAP kinase; cytosolic; cardiovascular-gen.; cardiac;  
XX vasoactive; hypotensive; antiarteriosclerotic; antiinflammatory;  
XX antiallergic; immunosuppressive; antibacterial; antispasmodic;  
XX dermatological; antidiabetic; gastrointestinal-gen.; antitumor;  
XX thrombolytic; neuroprotective; ophthalmological; antihemetic;  
XX antipyretic; uropathic; antiparasitic; hepatotropic; antianemic;  
XX muscular-gen.; thyromimetic; antihypertensive; nephrotoxic;  
XX hepatotropic; virucide; anti-HIV; anabolic; hypertensive; anorectic;  
XX endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anticonvulsant;  
XX antidepressant; antidiabetic; sedative; hypnotic; CNS-gen.;  
XX antifertility; cancer; cardiovascular disease; inflammation;  
XX metabolic disorder; neuropathy; sleep disorder.

XX Homo sapiens.

XX PN WO200507090-A2.

XX PD 27-JAN-2005.

XX PF 02-JUL-2004; 2004WO-US021514.

XX PR 03-JUL-2003; 2003US-0484761P.

XX PA (HARD ) HARVARD COLLEGE.

XX PI Blenis J, Murphy LO;

XX DR WPI, 2005-112720/12.

XX FT Identification of compound for treating e.g. cancer by culturing cells  
XX PT expressing target protein in the presence of growth factor, cytokine,  
XX PT tumor promoter or oncogene and assessing binding after contacting with  
XX the compound.

PS Claim 14; Page 64; 104pp; English.

XX The invention relates to a novel method for the identification of a  
XX therapeutic compound. The method involves providing test cells that  
XX express a target protein containing a DEF domain and MAP kinase;  
XX culturing the cells in the presence of growth factor, cytokine, tumor  
XX promoter or oncogene; contacting the cells with a candidate compound; and  
XX assessing the binding of the MAP kinase to the DEF domain relative to the  
XX binding in the absence of the candidate compound. The invention further  
XX comprises a method for the identification of a therapeutic compound; a  
XX method for treatment of cancer, which involves administering a compound  
XX that inhibits the binding of a MAP kinase to the DEF domain of a target  
XX protein; and an antibody that specifically binds to phospho-T-325 c-Fos  
XX (preferably polyclonal or monoclonal). The novel therapeutic compounds  
XX have the following activities: cytosolic; cardiovascular-gen.; cardiac;  
XX vasoactive; hypotensive; antiarteriosclerotic; antiinflammatory;  
XX antiallergic; immunosuppressive; antibacterial; antispasmodic;  
XX dermatological; antidiabetic; gastrointestinal-gen.; antitumor;  
XX thrombolytic; neuroprotective; ophthalmological; antihemetic;  
XX antipyretic; uropathic; antiparasitic; hepatotropic; antianemic; muscular  
XX -gen.; thyromimetic; antihypertensive; nephrotoxic;  
XX hepatotropic; virucide; anti-HIV; anabolic; hypertensive; anorectic;  
XX endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anticonvulsant;  
XX antidepressant; antidiabetic; sedative; hypnotic; CNS-gen.; and  
XX antifertility. The therapeutic compound may be used in the treatment  
XX of: cancer, cardiovascular disorders, inflammatory disorders, metabolic  
XX disorders, neuropathy or a behavioural disorder, and a sleep disorder.  
XX This sequence represents a metabolic therapy target peptide of the  
XX invention.

XX Sequence 15 AA;

Query Match 33.5%; Score 32.5; DB 9; Length 15;

Best Local Similarity 66.7%; Pred. No. 3.4e+02;  
Matches 8; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 5 KATNIFPYTPARG 16  
||| |||||  
DB 1 KAT--PYTPPG 9

RESULT 10

AAU76520

ID AAU76520 standard; peptide; 9 AA.

XX AC AAU76520;

DT 05-JUN-2002 (first entry)

XX DE Anti-Interleukin-12 (IL-12) antibody CDR3 light chain.

XX Human; antibody; anti-interleukin-12; CDR; light chain; circulatory;  
XX complementarity determining region; neuroprotective; antispasmodic;  
XX immunostimulant; cytosolic; anti-microbial; psoriasis; infection;  
XX multiple sclerosis; immune disorder; cardiovascular; malignant disease;  
XX neurological disorder.

XX Homo sapiens.

XX PN WO200212500-A2.

XX PD 14-FEB-2002.

XX PF 07-AUG-2001; 2001WO-US024720.

XX PR 07-AUG-2000; 2000US-0223358P.

XX PR 29-SEP-2000; 2000US-0236827P.

XX PR 01-AUG-2001; 2001US-00920262.

XX PA (CENZ ) CENTOCOR INC.

XX PI Giles-Komar J, Knight DM, Perlett D, Scallion B, Shealy D;

DR WPI: 2002-257482/30.

XX New mammalian anti-IL-12 antibodies, useful for diagnosing or treating IL

PT -12 related conditions, e.g. psoriasis or multiple sclerosis, as well as

PT other for treating immune, infectious, malignant or neurological

PT disorders.

XX Claim 41; Page 93; 96pp; English.

XX The invention relates to novel isolated mammalian anti-interleukin-12 (IL

CC -12) antibodies. The antibodies comprise at least one complementarity

CC determining region (CDR) of a heavy or light chain, a heavy chain or

CC light chain variable region, or a heavy chain or light chain constant

CC region. The anti-IL-12 antibodies are useful in methods for diagnosing or

CC treating IL-12 related conditions, e.g. psoriasis or multiple sclerosis.

CC The antibodies are also useful for treating immune, cardiovascular,

CC infectious, malignant or neurological disorders or diseases. The present

CC sequence represents the amino acid sequence of human anti-interleukin-12

CC (IL-12) antibody CDR3 light chain

XX

SO Sequence 9 AA:

Query Match 33.0%; Score 32; DB 5; Length 9;

Best Local Similarity 83.3%; Pred. No. 2.1e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 NIPYPT 13

DB 4 NIPYPT 9

RESULT 11

AAE15818

ID AAE15818 standard; peptide; 9 AA.

XX

AC AAE15818;

XX

DT 26-MAR-2002 (first entry)

XX

DE Human mAb 12B1 VK complementarity determining region (CDR) #3.

XX

KW Human; sialoadhesin factor-3; SAF-3; therapy; cancer; inflammation;

KW autoimmunity; allergy; asthma; infection; central nervous system; CNS;

KW rheumatoid arthritis; multiple sclerosis; stem cell mobilisation; AIDS;

KW haematopoietic development; anaemia; chemoprotective agent; cytotoxic;

KW immunoglobulin; complementarity determining region; CDR; protozoacide;

KW antiinflammatory; immunosuppressive; anti-HIV; antibacterial; virucide;

KW fungicide; neuroprotective; light chain variable region; VK; mAb;

KW monoclonal antibody.

XX

OS Homo sapiens.

XX

PN WO200190193-A1.

XX

PD 29-NOV-2001.

XX

PE 24-MAY-2001; 2001WO-US016864.

XX

PR 24-MAY-2000; 2000US-00577930.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX

PI Abrahamson JA, Kikly KK;

XX

DR WPI: 2002-083094/11.

XX

PT Novel monoclonal antibody that binds to human sialoadhesin factor-3 for

PT treating or preventing cancer, inflammation, autoimmunity, allergy,

PT asthma, rheumatoid arthritis, multiple sclerosis, AIDS and infections.

XX

PS Claim 13; Page 67; 69pp; English.

XX

CC The invention relates to monoclonal antibodies that bind to human

CC sialoadhesin factor-3 (SAF-3). SAF-3 antibody is useful for treating or

CC preventing cancer, inflammation, autoimmunity, allergy, asthma, central

CC nervous system (CNS) inflammation, rheumatoid arthritis, multiple

CC sclerosis, AIDS and bacterial, fungal, protozoan and viral infections and

CC for modulating an immune response in a mammal, where the immune response

CC is downregulated or enhanced. SAF-3 antibody is useful as diagnostic and

CC therapeutic reagents, to subcharacterise cell populations during

CC haematopoietic development, to treat anaemia, as a diagnostic marker to

CC distinguish between different forms of cancer, to purge bone marrow ex

CC vivo of cancer cells expressing SAF-3, as a tool to aid in the ex vivo

CC expansion (proliferation and/or differentiation) of haematopoietic

CC progenitor cells expressing SAF-3, as a stimulus in vivo for stem cell

CC mobilisation into the periphery and as an vivo chemoprotective agent.

CC Protein comprising immunoglobulin complementarity determining region

CC (CDR) of SAF-3 antibody and its nucleic acid is useful to configure

CC screening methods for detecting the effect of added compounds on the

CC production of mRNA and polypeptide in cells. The present sequence is

CC complementarity determining region of human monoclonal antibody (mAb)

CC 12B1 light chain variable region (VK), which binds to SAF-3

XX

SO Sequence 9 AA:

Query Match 33.0%; Score 32; DB 5; Length 9;

Best Local Similarity 83.3%; Pred. No. 2.1e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 NIPYPT 13

DB 4 NIPYPT 9

RESULT 12

AEF76312

ID AEF76312 standard; protein; 9 AA.

XX

AC AEF76312;

XX

DT 20-APR-2006 (first entry)

XX

DE Prostate cancer cell antibody light chain CDR3 SEQ ID NO:65.

XX

DE antibody; prostate tumor; cytostatic; andrology; genitourinary disease;

KW neoplasm; antibody identification; antibody therapy; light chain.

XX

OS Mus musculus.

XX

PN WO2006017173-A1.

XX

PD 16-FEB-2006.

XX

PE 08-JUL-2005; 2005WO-US024260.

XX

PR 10-JUL-2004; 2004US-0586811P.

XX

PA (ALEX-) ALEXION PHARM INC.

XX

PI Bowdish KS, Xin H, Vanciri F, Silva A;

XX

DR WPI: 2006-173528/18.

XX

PT New antibody that binds to a prostate cancer cell, useful for detecting

PT cancerous cells in vivo, for killing or ablating prostate cancer cells in

PT vivo, and for delivering a variety of cytotoxic drugs.

XX

PS Claim 16; SEQ ID NO 65; 48pp; English.

XX

CC The invention relates to an antibody (I) that binds to a prostate cancer

CC cell. Also described are the following: identifying (M) antibodies

CC specific to cancer cells; generating a phage displayed antibody library

CC using cells collected from subjects immunized with cancer cells, removing

CC members of the library that bind to human red blood cells to generate a

CC sub-library, and recovering from the sub-library members that display

CC antibodies that bind to the cancer cell; or contacting cancer cells with  
CC a hapten, generating a phage displayed antibody library using cells  
CC collected from subjects immunized with cancer cells, removing members of  
CC the library that bind to human red blood cells to generate a sub-library,  
CC and recovering from the sub-library members that display antibodies that  
CC bind to the cancer cell; an isolated nucleic acid (II) encoding (I); an  
CC expression vector (III) comprising (II); a host cell (IV) transfected  
CC with (III); and an antibody that binds to Cdcpl. (VI) is useful for  
CC identifying antibodies specific to cancer cells. (I) is useful as a  
CC therapeutic for cancer, for detecting cancerous cells in vivo, for  
CC killing or ablating cancerous cells in vivo (preferably prostate cancer  
CC cells), and for delivering a variety of cytotoxic drugs including  
CC therapeutic drugs, a compound emitting radiation, molecules of plants,  
CC fungal or bacterial origin, biological proteins, and their mixtures. The  
CC present sequence represents prostate cancer cell antibody light chain  
CC CDR3 SEQ ID NO:65.  
XX  
SQ Sequence 9 AA:  
Query Match 33.0%; Score 32; DB 10; Length 9;  
Best Local Similarity 83.3%; Pred. No. 2.1e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
OY 8 NIPPT 13  
DB 4 NIPPT 9  
RESULT 13  
ADT40399  
ID ADT40399 standard; peptide; 11 AA.  
XX  
AC ADT40399;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE hSARS virus peptide, SEQ ID 1387.  
XX  
KM Virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.  
XX  
OS SARS coronavirus.  
XX  
PN WO2004085650-A1.  
XX  
PD 07-OCT-2004.  
XX  
PF 24-MAR-2004; 2004WO-CN000246.  
XX  
PR 24-MAR-2003; 2003US-0457031P.  
XX  
PR 26-MAR-2003; 2003US-0457730P.  
XX  
PR 02-APR-2003; 2003US-0459931P.  
XX  
PR 03-APR-2003; 2003US-0460357P.  
XX  
PR 08-APR-2003; 2003US-0461265P.  
XX  
PR 14-APR-2003; 2003US-0462805P.  
XX  
PR 23-APR-2003; 2003US-0464886P.  
XX  
PR 25-APR-2003; 2003US-0465738P.  
XX  
PR 14-MAY-2003; 2003US-0470935P.  
XX  
PA (UYHK-) UNIV HONG KONG.  
XX  
PI Chan K, Guan Y, Nicholas JM, Peiris JSM, Poon L, Yuen K;  
XX  
PI Leung FC;  
XX  
DR WPI; 2004-737326/72.  
XX  
PT New nucleic acid molecule encoding nucleocapsid- or spike-gene protein of  
XX  
PT a human Severe Acute Respiratory Syndrome (hSARS) virus, useful for  
XX  
PT diagnosing and treating SARS.  
XX  
PS Example; SEQ ID NO 1387; 200P; English.  
XX  
CC The present invention relates to novel human Severe Acute Respiratory  
CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a

CC hSARS virus having China Center for Type Culture Collection Deposit  
CC Accession No. CCTCC-V200303. The present invention also relates to novel  
CC nucleic acid molecules (I; ADT41483 or ADT41485) encoding a nucleocapsid-  
CC (N) or spike (S)-gene protein of a hSARS virus. Also disclosed are  
CC methods for detecting the presence of a N- or S-gene of the hSARS virus  
CC or of the protein in a biological sample and identifying a subject  
CC infected with the hSARS virus. The hSARS virus, nucleic acid and protein  
CC sequences are useful as vaccines for diagnosing or treating SARS. They  
CC are also useful in clinical and scientific research applications. The  
CC hSARS virus genome (ADT39027) was obtained and the amino acid sequences  
CC of all three reading frames were deduced from the complementary strand.  
CC ADT40120 is the full-length protein encoded by the first reading frame of  
CC the complementary strand and ADT40121-ADT40601 are the peptides from the  
CC first reading frame protein. ADT40602 is the full-length protein encoded  
CC by the second reading frame of the complementary strand and ADT40603-  
CC ADT40976 are the peptides from the second reading frame protein. ADT40977  
CC is the full-length protein encoded by the third reading frame of the  
CC complementary strand and ADT40978-ADT41482 are the peptides from the  
CC third reading frame protein.  
XX  
SQ Sequence 11 AA:  
Query Match 33.0%; Score 32; DB 8; Length 11;  
Best Local Similarity 54.5%; Pred. No. 3e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
OY 3 GQKATNIPPT 13  
DB 1 GQSQSNILPPT 11  
RESULT 14  
ADT79816  
ID ADT79816 standard; protein; 11 AA.  
XX  
AC ADT79816;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE SARS virus complementary DNA strand reading frame 1 protein #279.  
XX  
KM Virucide; vaccine; detection; severe acute respiratory syndrome;  
XX  
KM real-time quantitative polymerase chain reaction; SARS.  
XX  
OS SARS coronavirus.  
XX  
PN WO2004085455-A1.  
XX  
PD 07-OCT-2004.  
XX  
PF 24-MAR-2004; 2004WO-CN000247.  
XX  
PR 24-MAR-2003; 2003US-0457031P.  
XX  
PR 26-MAR-2003; 2003US-0457730P.  
XX  
PR 02-APR-2003; 2003US-0459931P.  
XX  
PR 03-APR-2003; 2003US-0460357P.  
XX  
PR 08-APR-2003; 2003US-0461265P.  
XX  
PR 14-APR-2003; 2003US-0462805P.  
XX  
PR 23-APR-2003; 2003US-0464886P.  
XX  
PR 05-MAY-2003; 2003US-0468139P.  
XX  
PR 16-MAY-2003; 2003US-0471200P.  
XX  
PA (UYHK-) UNIV HONG KONG.  
XX  
PI Chan K, Guan Y, Nicholas JM, Peiris JSM, Poon L, Yuen K;  
XX  
PI WPI; 2004-737292/72.  
XX  
DR WPI; 2004-737292/72.  
XX  
PT New isolated nucleic acid molecule useful for detecting, treating,  
XX  
PT ameliorating, or preventing the virus causing severe acute respiratory  
XX  
PT syndrome in humans using a real-time quantitative polymerase chain  
XX  
PT reaction assay.  
XX

PS Example; SEQ ID NO 1387, 183pp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule consisting  
CC essentially of, and/or hybridizes under stringent conditions to a fully  
CC defined nucleotide sequence of 16-25 base pairs (bp); SEQ ID NO: 2471-  
CC 2476), or its complement. The methods and compositions of the present  
CC invention are useful for the detection of the virus causing Severe Acute  
CC Respiratory Syndrome (SARS) in humans using a real-time quantitative  
CC polymerase chain reaction (PCR) assay. They can also be used in treating,  
CC ameliorating, managing or preventing SARS. This sequence corresponds to a  
CC partial SARS protein sequence from the complementary reading frame 1.  
XX  
SQ Sequence 11 AA;  
Query Match 33.0%; Score 32; DB 8; Length 11;  
Best Local Similarity 54.5%; Pred. No. 3e+02; 4; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 3 GQKATNIFPYT 13  
Db 1 GOSOSNIIIPQT 11  
RESULT 15  
ADT37929  
ID ADT37929 standard; peptide; 11 AA.  
XX  
AC ADT37929;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE hSARS virus peptide, SEQ ID 1387.  
XX  
KW Virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.  
XX  
KM  
XX SARS coronavirus.  
XX OS  
XX MO2004085633-A1.  
XX PN  
XX 07-OCT-2004.  
XX PD  
XX 24-MAR-2004; 2004MO-CN000248.  
XX PF  
XX 24-MAR-2003; 2003US-0457031P.  
XX PR 26-MAR-2003; 2003US-0457730P.  
XX PR 02-APR-2003; 2003US-0459931P.  
XX PR 03-APR-2003; 2003US-0460357P.  
XX PR 08-APR-2003; 2003US-0461265P.  
XX PR 14-APR-2003; 2003US-0462805P.  
XX PR 23-APR-2003; 2003US-0464886P.  
XX  
XX (UYHK-) UNIV HONG KONG.  
XX  
XX Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K,  
XX PI Leung PC;  
XX  
XX WPI; 2004-728736/71.  
XX  
XX  
XX New isolated human severe acute respiratory syndrome (hSARS) virus,  
XX PT useful as vaccine for diagnosing or treating SARS or in clinical and  
XX PT scientific research applications.  
XX  
XX  
XX Example; SEQ ID NO 1387, 176pp; English.  
XX  
XX The present invention relates to novel human Severe Acute Respiratory  
XX Syndrome (hSARS) viral nucleic acid and protein sequences derived from a  
XX hSARS virus having China Center for Type Culture Collection Deposit  
XX Accession No. CCTCC-V200303. The hSARS virus, nucleic acid and protein  
XX sequences are useful as vaccines for diagnosing or treating SARS. They  
XX are also useful in clinical and scientific research applications. The  
XX hSARS virus genome (ADT36557) was obtained and the amino acid sequences  
XX of all three reading frames were deduced from the complementary strand of  
XX ADT37650 is the full-length protein encoded by the first reading frame of

CC the complementary strand and ADT37651-ADT38131 are the peptides from the  
CC first reading frame protein. ADT38132 is the full-length protein encoded  
CC by the second reading frame of the complementary strand and ADT38133-  
CC ADT38506 are the peptides from the second reading frame protein. ADT38507  
CC is the full-length protein encoded by the third reading frame of the  
CC complementary strand and ADT38508-ADT39012 are the peptides from the  
CC third reading frame protein.  
XX  
XX  
SQ Sequence 11 AA;  
Query Match 33.0%; Score 32; DB 8; Length 11;  
Best Local Similarity 54.5%; Pred. No. 3e+02; 4; Indels 0; Gaps 0;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
QY 3 GQKATNIFPYT 13  
Db 1 GOSOSNIIIPQT 11  
Search completed: May 30, 2006, 15:04:08  
Job time : 61.6667 secs



GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 30, 2006, 15:17:23 ; Search time 49.3333 Seconds  
(without alignments)  
169.011 Million cell updates/sec

Title: US-10-758-165A-10  
Sequence: 1 VDGQKATNIPFYTPAGKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues  
Total number of hits satisfying chosen parameters: 432914

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US10A\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	97	100.0	18	5	US-10-758-165-10 Sequence 10, Appl
2	87	89.7	18	5	US-10-758-165-9 Sequence 9, Appl
3	55	56.7	18	5	US-10-758-165-12 Sequence 12, Appl
4	37	38.1	15	5	US-10-836-118-34 Sequence 34, Appl
5	35	36.1	18	5	US-10-758-165-11 Sequence 11, Appl
6	34	35.1	15	4	US-10-052-788-5 Sequence 5, Appl
7	32	33.0	9	3	US-09-920-262A-6 Sequence 6, Appl
8	32	33.0	9	5	US-10-912-994-6 Sequence 6, Appl
9	32	33.0	9	5	US-10-975-883-6 Sequence 6, Appl
10	32	33.0	9	5	US-10-975-740A-6 Sequence 6, Appl
11	32	33.0	9	5	US-10-975-708-6 Sequence 6, Appl
12	32	33.0	9	5	US-10-246-019A-14 Sequence 14, Appl
13	32	33.0	11	5	US-10-807-887-1387 Sequence 1387, Ap
14	32	33.0	11	6	US-10-807-887-1387 Sequence 1387, Ap
15	32	33.0	11	6	US-11-004-399-2080 Sequence 2080, Ap
16	32	33.0	15	4	US-10-107-532-5915 Sequence 5915, Ap
17	32	33.0	15	4	US-10-107-532-5915 Sequence 5915, Ap
18	32	33.0	15	4	US-10-107-532-5915 Sequence 5915, Ap
19	32	33.0	15	4	US-10-107-532-5915 Sequence 5915, Ap
20	32	33.0	15	4	US-10-107-532-5915 Sequence 5915, Ap
21	32	33.0	15	4	US-10-107-532-5915 Sequence 5915, Ap
22	32	33.0	15	4	US-10-107-532-5915 Sequence 5915, Ap
23	32	33.0	15	4	US-10-107-532-5915 Sequence 5915, Ap
24	32	33.0	15	4	US-10-107-532-5915 Sequence 5915, Ap
25	32	33.0	15	4	US-10-107-532-5915 Sequence 5915, Ap
26	32	33.0	15	4	US-10-107-532-5915 Sequence 5915, Ap
27	32	33.0	15	4	US-10-107-532-5915 Sequence 5915, Ap

28	29	29.9	9	6	US-11-009-040A-214 Sequence 214, App
29	29	29.9	9	6	US-11-009-073A-214 Sequence 214, App
30	29	29.9	9	6	US-11-009-769A-214 Sequence 214, App
31	29	29.9	12	3	US-09-813-653-26 Sequence 26, Appl
32	29	29.9	15	5	US-10-865-478-786 Sequence 786, App
33	29	29.9	15	5	US-10-720-831-70 Sequence 70, Appl
34	29	29.9	17	4	US-10-306-631-76 Sequence 76, Appl
35	29	29.9	18	4	US-10-654-200-28 Sequence 28, Appl
36	29	29.9	18	4	US-10-654-200-29 Sequence 29, Appl
37	29	29.9	18	5	US-10-846-548A-1 Sequence 1, Appl
38	28	28.9	9	4	US-10-160-506-34 Sequence 34, Appl
39	28	28.9	9	4	US-10-449-379-34 Sequence 34, Appl
40	28	28.9	9	4	US-10-688-015-34 Sequence 34, Appl
41	28	28.9	9	4	US-10-160-505-34 Sequence 34, Appl
42	28	28.9	9	5	US-10-482-284A-186 Sequence 186, App
43	28	28.9	9	6	US-11-218-813-34 Sequence 34, Appl
44	28	28.9	10	4	US-10-281-652-18 Sequence 18, Appl
45	28	28.9	10	5	US-10-691-157-18 Sequence 18, Appl

ALIGNMENTS

RESULT 1  
US-10-758-165-10  
; Sequence 10, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammeberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-10-758-165-10

Query Match 100.0%; Score 97; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 6.2e-09;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIPFYTPAGKQ 18  
Db 1 VDGQKATNIPFYTPAGKQ 18  
RESULT 2  
US-10-758-165-9  
; Sequence 9, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammeberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10758,165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-10-758-165-9  
Query Match 89.7%; Score 87; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.9e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDGOATNIPFYTAP 16  
Db 1 VDGOATNIPFYTAP 16

## RESULT 3

US-10-758-165-12  
; Sequence 12, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 12  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-10-758-165-12

Query Match 56.7%; Score 55; DB 5; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.061;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 VDGOATNIPFYTAP 15  
Db 1 VDGOEDRNLFSTYAP 15

## RESULT 4

US-10-856-118-34  
; Sequence 34, Application US/10856118  
; Publication No. US20050025747A1  
; GENERAL INFORMATION:  
; APPLICANT: Laidlaw, Stephen  
; APPLICANT: Skinner, Mike  
; APPLICANT: Hill, Adrian V.S.  
; APPLICANT: Gilbert, Sarah C.  
; APPLICANT: Anderson, Richard  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: 3742.1000-000  
; CURRENT APPLICATION NUMBER: US/10/856,118  
; CURRENT FILING DATE: 2004-05-27  
; PRIOR APPLICATION NUMBER: PCT/GB02/005411  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: GB0128733.3  
; PRIOR FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: US 60/334,649  
; PRIOR FILING DATE: 2001-11-30  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flanking sequence  
US-10-856-118-34

Query Match 38.1%; Score 37; DB 5; Length 15;  
Best Local Similarity 55.6%; Pred. No. 50;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 7 TNIFPYTAP 15  
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Db 2 TNVYPYDVP 10

## RESULT 5

US-10-758-165-11  
; Sequence 11, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 11  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Equus caballus  
US-10-758-165-11

Query Match 36.1%; Score 35; DB 5; Length 18;  
Best Local Similarity 44.4%; Pred. No. 1.3e+02;  
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

OY 1 VDGOATNIPFYTAPGKQ 18  
Db 1 IDGQKVDEQFPQHGVLVKQ 18

## RESULT 6

US-10-052-788-5  
; Sequence 5, Application US/10052788  
; Publication No. US20030087314A1  
; GENERAL INFORMATION:  
; APPLICANT: Gerahwin, Laurel J.  
; APPLICANT: Pettigrew, Howard David  
; APPLICANT: Kalina, Warren V.  
; APPLICANT: The Regents of the University of California  
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for  
; FILE REFERENCE: 023070-121000US  
; CURRENT APPLICATION NUMBER: US/10/052,788  
; CURRENT FILING DATE: 2001-11-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: epitope peptide  
; OTHER INFORMATION: p5, middle portion of C2 of equine IGF epsilon  
; OTHER INFORMATION: heavy chain  
US-10-052-788-5

Query Match 35.1%; Score 34; DB 4; Length 15;  
Best Local Similarity 54.5%; Pred. No. 1.6e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 VDGOATNIPFP 11  
Db 2 IDGQKVDEQFP 12

## RESULT 7

US-09-920-262A-6  
; Sequence 6, Application US/09920262A  
; Publication No. US20030124123A1  
; GENERAL INFORMATION:  
; APPLICANT: Shealy, David

```

; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920,262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-262A-6
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Query Match          33.0%; Score 32; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY      8 NIPYPT 13
      ||:||||
Db      4 NIPYPT 9
```

```

RESULT 8
US-10-912-994-6
; Sequence 6, Application US/10912994
; Publication No. US2005002937A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Knight, David
; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248DIV1
; CURRENT APPLICATION NUMBER: US/10/912,994
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-912-994-6
```

```
Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 NIPYPT 13
      ||:||||
Db      4 NIPYPT 9
```

```

RESULT 9
US-10-975-883-6
; Sequence 6, Application US/10975883
; Publication No. US20050112127A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Knight, David
```

```

; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND USES
; FILE REFERENCE: CEN0248DIV04
; CURRENT APPLICATION NUMBER: US/10/975,883
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-883-6
```

```
Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 NIPYPT 13
      ||:||||
Db      4 NIPYPT 9
```

```

RESULT 10
US-10-975-740A-6
; Sequence 6, Application US/10975740A
; Publication No. US20050196838A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Knight, David
; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND NUCLEIC ACIDS
; FILE REFERENCE: CEN0248DIV03
; CURRENT APPLICATION NUMBER: US/10/975,740A
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-740A-6
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```
Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 NIPYPT 13
      ||:||||
Db      4 NIPYPT 9
```

```

RESULT 11
US-10-975-708-6
; Sequence 6, Application US/10975708
; Publication No. US20050214293A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
```

```

; APPLICANT: Knight, David
; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND COMPOSITIONS
; FILE REFERENCE: CEN0248DIV02
; CURRENT APPLICATION NUMBER: US/10/975,708
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-708-6
```

```

Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 NIPYPT 13
      ||:||||
Db      4 NIPYPT 9
```

```

RESULT 12
US-10-246-019A-14
; Sequence 14, Application US/10246019A
; Publication No. US20060073133A1
; GENERAL INFORMATION:
; APPLICANT: Kikly, Kristine K.
; APPLICANT: Abrahamson, Julie
; TITLE OF INVENTION: Sialoadhesin Factor-3 Antibodies
; FILE REFERENCE: GHS0019-1C1
; CURRENT APPLICATION NUMBER: US/10/246,019A
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: US9N 09/577,930
; PRIOR FILING DATE: 2000-01-22
; PRIOR APPLICATION NUMBER: US9N 09/046,736
; PRIOR FILING DATE: 1998-03-24
; PRIOR APPLICATION NUMBER: US9N 60/041,885
; PRIOR FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human
US-10-246-019A-14
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```

Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY      8 NIPYPT 13
      ||:||||
Db      4 NIPYPT 9
```

```

RESULT 13
US-10-808-187-1387
; Sequence 1387, Application US/10808187
; Publication No. US2005009009A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
```

```

; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1387
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-1387
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```

Query Match          33.0%; Score 32; DB 5; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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```
QY      3 GOKATNIPYPT 13
      ||:||||
Db      1 GOSOSNIPPT 11
```

```

RESULT 14
US-10-807-807-1387
; Sequence 1387, Application US/10807807
; Publication No. US20050181357A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; FILE REFERENCE: V9661.0077
; CURRENT APPLICATION NUMBER: US/10/807,807
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/464,886
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; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/465,738
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/470,935
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1387
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-807-807-1387

```

```

Query Match          33.0%; Score 32; DB 5; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      3 GOKATNIFPYT 13
      ||:|||||
Db      1 GQSQSNIIPQT 11

```

```

RESULT 15
US-11-004-399-2080
; Sequence 2080, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sachiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peirib, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-Cov Viral Nucleotide
; FILE REFERENCE: 2587/73166/RDX
; CURRENT APPLICATION NUMBER: US/11/004,399
; PRIOR FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2080
; LENGTH: 11
; TYPE: PRT
; ORGANISM: SARS-Cov Virus
US-11-004-399-2080

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Query Match          33.0%; Score 32; DB 6; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```

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QY      3 GOKATNIFPYT 13
      ||:|||||
Db      1 GQSQSNIIPQT 11

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Search completed: May 30, 2006, 15:20:14
Job time : 49.3333 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 30, 2006, 15:17:53 ; Search time 4 Seconds  
(without alignments)  
50.118 Million cell updates/sec

Title: US-10-758-165A-10  
Perfect score: 97  
Sequence: 1 VDGKATNIFPYTPGKQ 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 11661

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA New:\*  
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3: /EMC\_CeJelerra\_SIDS3/ptodaca/1/pubppaa/US07\_NEW\_PUB.pep:\*  
4: /EMC\_CeJelerra\_SIDS3/ptodaca/1/pubppaa/US08\_NEW\_PUB.pep:\*  
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6: /EMC\_CeJelerra\_SIDS3/ptodaca/1/pubppaa/US10\_NEW\_PUB.pep:\*  
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8: /EMC\_CeJelerra\_SIDS3/ptodaca/1/pubppaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28.9	9	7	US-11-219-563-34	Sequence 34, Appl
2	26.8	9	7	US-11-254-182-12	Sequence 12, Appl
3	25.8	12	7	US-11-177-358C-16	Sequence 16, Appl
4	25.8	12	7	US-11-177-359C-16	Sequence 16, Appl
5	25.8	12	7	US-11-177-340C-16	Sequence 16, Appl
6	24.7	10	6	US-10-538-066-747	Sequence 747, App
7	24.7	16	1	US-09-731-899-19	Sequence 19, Appl
8	23.7	9	6	US-10-522-356-3	Sequence 3, Appl1
9	23.7	9	7	US-11-252-276-38	Sequence 38, Appl
10	23.7	9	7	US-11-023-959A-83	Sequence 83, Appl
11	23.7	10	7	US-11-140-487A-1314	Sequence 1314, Ap
12	23.7	12	7	US-11-106-014-82	Sequence 82, Appl
13	23.7	13	7	US-11-134-228A-8	Sequence 8, Appl1
14	23.7	17	7	US-11-251-734-50	Sequence 30, Appl
15	23.2	12	7	US-11-122-966-799	Sequence 799, App
16	22.7	9	7	US-11-297-317-21	Sequence 21, Appl
17	22.7	9	7	US-11-140-487A-211	Sequence 211, App
18	22.7	9	7	US-11-140-487A-348	Sequence 348, App
19	22.7	10	7	US-11-140-487A-1346	Sequence 1346, Ap
20	22.7	13	7	US-11-219-563-10	Sequence 39, Appl
21	22.7	14	7	US-11-219-563-10	Sequence 39, Appl
22	22.7	14	7	US-11-300-563-8	Sequence 8, Appl1
23	22.7	16	7	US-11-122-986-812	Sequence 812, App
24	22.7	17	7	US-11-251-498-59	Sequence 59, Appl
25	22.7	17	7	US-11-121-282-52	Sequence 52, Appl

26	22	22.7	18	7	US-11-257-498-53	Sequence 53, Appl
27	21	21.6	9	7	US-11-055-093-222	Sequence 222, App
28	21	21.6	9	7	US-11-140-487A-120	Sequence 120, App
29	21	21.6	9	7	US-11-140-487A-551	Sequence 551, App
30	21	21.6	9	7	US-11-140-487A-1446	Sequence 1446, Ap
31	21	21.6	10	7	US-11-055-093-223	Sequence 223, App
32	21	21.6	10	7	US-11-140-487A-1447	Sequence 1447, Ap
33	21	21.6	10	7	US-11-140-487A-1596	Sequence 1596, Ap
34	21	21.6	11	6	US-10-540-431-11	Sequence 11, Appl
35	21	21.6	11	7	US-11-177-358C-3	Sequence 3, Appl1
36	21	21.6	11	7	US-11-177-359C-3	Sequence 3, Appl1
37	21	21.6	11	7	US-11-177-340C-3	Sequence 3, Appl1
38	21	21.6	11	7	US-11-122-986-800	Sequence 800, App
39	21	21.6	12	1	US-09-784-950-21	Sequence 21, Appl
40	21	21.6	12	7	US-11-122-986-656	Sequence 656, App
41	21	21.6	13	7	US-11-211-175-1	Sequence 1, Appl1
42	20	20.6	9	7	US-11-140-487A-8	Sequence 8, Appl1
43	20	20.6	9	7	US-11-140-487A-24	Sequence 24, Appl
44	20	20.6	9	7	US-11-140-487A-212	Sequence 212, App
45	20	20.6	9	7	US-11-140-487A-327	Sequence 327, App

## ALIGNMENTS

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RESULT 1
US-11-219-563-34
; Sequence 34, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bandier, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219, 563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379, 838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449, 379
; PRIOR FILING DATE: 2003-05-10
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatsSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-219-563-34
;
;
;
Query Match 28.9%; Score 28; DB 7; Length 9;
Best Local Similarity 63.6%; Pred. NO. 5.2e+04;
Matches 7; Conservative 0; Mismatches 2; Gaps 1;
Indels 1;
OY 3 GOKATNIFPYT 13
Db 1 GOSTY--FPYT 9
RESULT 2
US-11-254-182-12
; Sequence 12, Application US/11254182
; Publication No. US20060088523A1
; GENERAL INFORMATION:
; APPLICANT: ANDYA, JAMES
; APPLICANT: GME, SHIANG C.
; APPLICANT: LIU, JUN
; APPLICANT: SHEN, YE
; TITLE OF INVENTION: ANTIBODY FORMULATIONS
; FILE REFERENCE: P2104R1
; CURRENT APPLICATION NUMBER: US/11/254, 182
; CURRENT FILING DATE: 2005-10-19
; PRIOR APPLICATION NUMBER: US 60/620, 413
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PRIOR FILING DATE: 2004-10-20  
NUMBER OF SEQ ID NOS: 74  
SEQ ID NO 12  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: sequence is synthesized  
US-11-254-182-12

Query Match 26.8%; Score 26; DB 7; Length 9;  
Best Local Similarity 80.0%; Pred. No. 5.2e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 IFPYT 13  
|:|:|  
Db 5 IVPYT 9

RESULT 3  
US-11-177-358C-16  
Sequence 16, Application US/11177358C  
Publication No. US20060094072A1  
GENERAL INFORMATION:  
APPLICANT: CAMPBELL, DOUGLAS A.  
TITLE OF INVENTION: PEPTIDE SEQUENCE TAGS AND METHOD OF USING SAME  
FILE REFERENCE: 113703-1006  
CURRENT APPLICATION NUMBER: US/11/177,358C  
CURRENT FILING DATE: 2005-07-11  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 16  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
US-11-177-358C-16

Query Match 25.8%; Score 25; DB 7; Length 12;  
Best Local Similarity 50.0%; Pred. No. 94;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 FPYTAPGK 17  
|:|:|  
Db 1 FPCDGPGR 8

RESULT 4  
US-11-177-359C-16  
Sequence 16, Application US/11177359C  
Publication No. US20060094058A1  
GENERAL INFORMATION:  
APPLICANT: CAMPBELL, DOUGLAS A.  
TITLE OF INVENTION: PEPTIDE SEQUENCE TAGS AND METHOD OF USING SAME  
FILE REFERENCE: 113703-1004  
CURRENT APPLICATION NUMBER: US/11/177,359C  
CURRENT FILING DATE: 2005-07-11  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 16  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
US-11-177-359C-16

Query Match 25.8%; Score 25; DB 7; Length 12;  
Best Local Similarity 50.0%; Pred. No. 94;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 FPYTAPGK 17

Db 1 FPCDGPGR 8

RESULT 5  
US-11-177-340C-16  
Sequence 16, Application US/11177340C  
Publication No. US20060099663A1  
GENERAL INFORMATION:  
APPLICANT: CAMPBELL, DOUGLAS A.  
TITLE OF INVENTION: PEPTIDE SEQUENCE TAGS AND METHOD OF USING SAME  
FILE REFERENCE: 113703-1005  
CURRENT APPLICATION NUMBER: US/11/177,340C  
CURRENT FILING DATE: 2005-07-11  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 16  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
US-11-177-340C-16

Query Match 25.8%; Score 25; DB 7; Length 12;  
Best Local Similarity 50.0%; Pred. No. 94;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 FPYTAPGK 17  
|:|:|  
Db 1 FPCDGPGR 8

RESULT 6  
US-10-538-066-747  
Sequence 747, Application US/10538066  
Publication No. US20060094649A1  
GENERAL INFORMATION:  
APPLICANT: Epimmune Inc.  
TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen  
FILE REFERENCE: 2060.015PC06  
CURRENT APPLICATION NUMBER: US/10/538,066  
CURRENT FILING DATE: 2005-06-09  
PRIOR APPLICATION NUMBER: US 60/432,017  
PRIOR FILING DATE: 2002-12-10  
NUMBER OF SEQ ID NOS: 767  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 747  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: A3 non-natural consensus peptide  
US-10-538-066-747

Query Match 24.7%; Score 24; DB 6; Length 10;  
Best Local Similarity 44.4%; Pred. No. 1.1e+02;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 IFPYTAPGK 17  
|:|:|  
Db 2 VFYPALINK 10

RESULT 7  
US-09-731-899-19  
Sequence 19, Application US/09731899  
Publication No. US20060088548A1  
GENERAL INFORMATION:  
APPLICANT: Chaim, Benjamin  
TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THERETO, AND METHODS  
FOR IMMUNIZATION USING CHIMERIC PEPTIDES OR ANTIBODIES



Wed May 31 06:05:16 2006

us-10-758-165a-10.closed.rapbn

FILE REFERENCE: 20555/1203433-US1  
CURRENT APPLICATION NUMBER: US/09/771,899  
CURRENT FILING DATE: 2000-12-08  
PRIOR APPLICATION NUMBER: 60/169,687  
PRIOR FILING DATE: 1999-12-08  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 19  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Tetanus toxin bacteria  
US-09-731-899-19

Query Match 24.7%; Score 24; DB 1; Length 16;  
Best Local Similarity 44.4%; Pred. No. 1.9e+02;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 7 TNYFYTAP 15  
DB 3 STYVYIGP 11

RESULT 8  
US-10-522-356-3

Sequence 3, Application US/10522356  
Publication No. US20060105323A1  
GENERAL INFORMATION:  
APPLICANT: WHITEHEAD, CHRISTOPHER BRUCE ALEXANDER  
APPLICANT: CLARK, ANTHONY JOHN  
TITLE OF INVENTION: MULTI-REPORTER GENE MODEL FOR TOXICOLOGICAL SCREENING  
FILE REFERENCE: 102286.155 US1  
CURRENT APPLICATION NUMBER: US/10/522.356  
CURRENT FILING DATE: 2005-01-26  
PRIOR APPLICATION NUMBER: PCT/GB03/003192  
PRIOR FILING DATE: 2003-07-25  
PRIOR APPLICATION NUMBER: GB 0217402.7  
PRIOR FILING DATE: 2002-07-26  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 3  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: Description of Unknown Sequence: Haemagglutinin  
US-10-522-356-3

Query Match 23.7%; Score 23; DB 6; Length 9;  
Best Local Similarity 50.0%; Pred. No. 5.2e+04;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 10 FPYTAP 15  
DB 1 YPYDVP 6

RESULT 9  
US-11-252-276-38

Sequence 38, Application US/11252276  
Publication No. US20060094868A1  
GENERAL INFORMATION:  
APPLICANT: Giuliano, Kenneth A.  
APPLICANT: Bright, Gary  
APPLICANT: Olson, Keith  
APPLICANT: Burroughs-Tencza, Sarah  
TITLE OF INVENTION: A System for Cell Based Screening  
FILE REFERENCE: 97-022-K2-CO  
CURRENT APPLICATION NUMBER: US/11/252.276  
CURRENT FILING DATE: 2005-10-17  
PRIOR APPLICATION NUMBER: 09/713,572  
PRIOR FILING DATE: 2000-11-15

PRIOR APPLICATION NUMBER: 09/430,656  
PRIOR FILING DATE: 1999-10-29  
PRIOR APPLICATION NUMBER: 09/398,965  
PRIOR FILING DATE: 1999-09-17  
PRIOR APPLICATION NUMBER: 09/031,271  
PRIOR FILING DATE: 1998-02-27  
PRIOR APPLICATION NUMBER: 08/810,983  
PRIOR FILING DATE: 1997-02-27  
PRIOR APPLICATION NUMBER: 60/136,078  
PRIOR FILING DATE: 1999-05-26  
PRIOR APPLICATION NUMBER: 60/106,308  
PRIOR FILING DATE: 1998-10-30  
NUMBER OF SEQ ID NOS: 168  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 38  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: HA epitope  
US-11-252-276-38

Query Match 23.7%; Score 23; DB 7; Length 9;  
Best Local Similarity 50.0%; Pred. No. 5.2e+04;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 10 FPYTAP 15  
DB 1 YPYDVP 6

RESULT 10  
US-11-023-959A-83  
Sequence 83, Application US/11023959A  
Publication No. US20060106203A1  
GENERAL INFORMATION:  
APPLICANT: Winter, Greg  
TITLE OF INVENTION: Ligand  
FILE REFERENCE: 8039/2142  
CURRENT APPLICATION NUMBER: US/11/023.959A  
CURRENT FILING DATE: 2004-12-28  
PRIOR APPLICATION NUMBER: PCT/GB03/002804  
PRIOR FILING DATE: 2003-06-30  
NUMBER OF SEQ ID NOS: 187  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 83  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: HA tag  
US-11-023-959A-83

Query Match 23.7%; Score 23; DB 7; Length 9;  
Best Local Similarity 50.0%; Pred. No. 5.2e+04;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 10 FPYTAP 15  
DB 1 YPYDVP 6

RESULT 11  
US-11-140-487A-1314  
Sequence 1314, Application US/11140487A  
Publication No. US20060093617A1  
GENERAL INFORMATION:  
APPLICANT: Innogenetics N.V.  
TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C v.  
FILE REFERENCE: 166  
CURRENT APPLICATION NUMBER: US/11/140.487A  
CURRENT FILING DATE: 2005-05-31  
PRIOR APPLICATION NUMBER: EP 04012951.2

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; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1314
; LENGTH: 10
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-1314
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Query Match
Best Local Similarity 23.7%; Score 23; DB 7; Length 10;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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Qy 9 IFPTAPGKQ 18
Db 1 IYRVTYGER 10
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RESULT 12
US-11-106-014-82
; Sequence 82, Application US/11106014
; Publication No. US2006008846A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, Michele
; APPLICANT: Chiari, Dan Sharim
; APPLICANT: Laties, Esther
; APPLICANT: Stivasca, Promod
; APPLICANT: Chandawarkar, Rajiv
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT
; FILE REFERENCE: 5914-106-999
; CURRENT APPLICATION NUMBER: US/11/106,014
; PRIOR FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 10/632,150
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1997-03-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 82
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-014-82
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Query Match
Best Local Similarity 23.7%; Score 23; DB 7; Length 12;
Matches 6; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
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RESULT 13

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Qy 2 DGQATIFPYTA 14
Db 2 DGEKDT--YSYLA 12
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US-11-134-228A-8
; Sequence 8, Application US/11134228A
; Publication No. US20060105320A1
; GENERAL INFORMATION:
; APPLICANT: Lindquist et al
; TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS
; FILE REFERENCE: 30554/40155A
; CURRENT APPLICATION NUMBER: US/11/134,228A
; PRIOR FILING DATE: 2005-05-20
; PRIOR FILING DATE: 2004-05-20
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hemagglutinin
US-11-134-228A-8
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Query Match
Best Local Similarity 23.7%; Score 23; DB 7; Length 13;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 10 FPYVAP 15
Db 1 YPVDVP 6
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RESULT 14
US-11-251-734-30
; Sequence 30, Application US/11251734
; Publication No. US20060100134A1
; GENERAL INFORMATION:
; APPLICANT: AVENTIS PHARMACEUTICALS INC.
; APPLICANT: GUO, Yong
; APPLICANT: MORSE, Clarence C
; APPLICANT: YAO, Zhengbin
; TITLE OF INVENTION: MEMBRANE PENETRATING PEPTIDES AND USES THEREOF
; FILE REFERENCE: HMR2053 US NPI
; CURRENT APPLICATION NUMBER: US/11/251,734
; PRIOR FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US 09/933,780
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,647
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: GB 0103110.3
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-11-251-734-30
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Query Match
Best Local Similarity 23.7%; Score 23; DB 7; Length 17;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Qy 5 KATNIF 10
Db 2 KKTNLF 7
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RESULT 15
US-11-122-986-799
; Sequence 799, Application US/1122986
; Publication No. US20060104989A1
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; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 799
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-11-122-986-799
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Query Match 23.2%; Score 22.5; DB 7; Length 12;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
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QY 7 TNFFPYTAPG 16
   :|||
Db 1 SNI-PYTMVG 9
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Search completed: May 30, 2006, 15:20:31  
Job time : 4 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2006, 15:08:01 ; Search time 19.333 Seconds  
(without alignments)  
81.494 Million cell updates/sec

Title: US-10-758-165A-9  
Perfect score: 97  
Sequence: 1 VDGQKATNIFPYTAPGTX 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 271358

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents\_AA:\*  
1: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/H\_COMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/PCITUS\_COMB.pep:\*  
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7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	33.0	9	2	US-09-920-262A-6
2	32	33.0	15	2	US-09-674-973A-64
3	30	30.9	9	2	US-09-865-548A-126
4	30	30.9	17	1	US-08-333-565-22
5	30	30.9	17	1	US-08-661-479-22
6	29	29.9	9	2	US-09-042-353-366
7	29	29.9	9	2	US-08-758-417A-214
8	29	29.9	11	2	US-09-307-265A-14
9	29	29.9	15	2	US-08-278-774-20
10	29	29.9	15	2	US-09-526-195-9
11	29	29.9	16	2	US-08-957-130-19
12	29	29.9	18	2	US-09-856-920-1
13	28	28.9	10	2	US-09-641-803-18
14	28	28.9	10	2	US-09-641-802-18
15	28	28.9	10	2	US-09-641-801-18
16	28	28.9	10	2	US-10-281-652-18
17	28	28.9	15	1	US-08-080-073-26
18	27	27.8	8	2	US-08-981-392-83
19	27	27.8	8	2	US-09-908-322-83
20	27	27.8	9	1	US-08-346-333-41
21	27	27.8	9	5	PCT-US91-07506-41
22	27	27.8	11	1	US-07-958-903A-5
23	27	27.8	11	1	US-08-462-018-5
24	27	27.8	11	1	US-08-823-245-5
25	27	27.8	11	2	US-07-963-329A-69
26	27	27.8	11	2	US-09-318-001-5

27	27	27.8	11	2	US-09-064-159-5	Sequence 5, Appli
28	27	27.8	11	2	US-09-809-417A-21	Sequence 21, Appl
29	27	27.8	11	5	PCT-US92-0943A-69	Sequence 69, Appl
30	27	27.8	13	1	US-07-958-903A-8	Sequence 8, Appli
31	27	27.8	13	1	US-08-462-018-8	Sequence 8, Appli
32	27	27.8	13	1	US-08-823-245-8	Sequence 8, Appli
33	27	27.8	13	2	US-07-963-329A-58	Sequence 58, Appl
34	27	27.8	13	2	US-09-318-001-8	Sequence 8, Appli
35	27	27.8	13	2	US-09-064-159-8	Sequence 8, Appli
36	27	27.8	13	5	PCT-US92-0943A-58	Sequence 58, Appl
37	27	27.8	17	1	US-08-325-553-9	Sequence 9, Appli
38	27	27.8	17	1	US-08-394-152A-9	Sequence 9, Appli
39	27	27.8	17	2	US-08-705-477E-9	Sequence 9, Appli
40	27	27.8	17	2	US-08-466-381C-9	Sequence 9, Appli
41	27	27.8	18	1	US-09-017-205-48	Sequence 48, Appl
42	27	27.8	18	1	US-09-017-205-49	Sequence 49, Appl
43	26.5	27.3	15	3	US-09-641-528B-474A0	Sequence 474A0, A
44	26.5	27.3	15	3	US-09-641-528B-47461	Sequence 47461, A
45	26	26.8	5	2	US-09-788-006-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1  
US-09-920-262A-6  
; Sequence 6, Application US/09920262A  
; Patent No. 6902734  
; GENERAL INFORMATION:  
; APPLICANT: Shealy, David  
; APPLICANT: Knight, David  
; APPLICANT: Scallion, Bernie  
; APPLICANT: Giles-Komar, Jill  
; APPLICANT: Peritt, David  
; TITLE OF INVENTION: Anti-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES  
; FILE REFERENCE: CEN0248  
; CURRENT APPLICATION NUMBER: US/09/920,262A  
; CURRENT FILING DATE: 2002-05-06  
; PRIOR APPLICATION NUMBER: 60/223,358  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: 60/236,827  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver 3.1  
; SEQ ID NO 6  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-920-262A-6  
  
Query Match 33.0% Score 32, DB 2, Length 9;  
Best Local Similarity 83.3% Pred. No. 5e+05;  
Matches 5, Conservative 1, Mismatches 0, Indels 0, Gaps 0;  
  
QY 8 NIPPT 13  
DB 4 NIPPT 9  
  
RESULT 2  
US-09-674-973A-64  
; Sequence 64, Application US/09674973A  
; Patent No. 6759046  
; GENERAL INFORMATION:  
; APPLICANT: No. 6759046ak Hydro ASA  
; TITLE OF INVENTION: Peptides  
; FILE REFERENCE: 26625-296  
; CURRENT APPLICATION NUMBER: US/09/674,973A  
; CURRENT FILING DATE: 2001-06-04  
; NUMBER OF SEQ ID NOS: 459  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 64  
; LENGTH: 15

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-674-973A-64

Query Match
Best Local Similarity 33.0%; Score 32; DB 2; Length 15;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 1 VDQKATNIFP 11
Db 4 VEDQKTLVFP 14

RESULT 3
US-09-865-548A-126
; Sequence 126, Application US/09865548A
; Patent No. 6867283
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arle
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 126
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-126

Query Match
Best Local Similarity 30.9%; Score 30; DB 2; Length 9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 NIFPY 12
Db 1 NIFPY 5

RESULT 4
US-08-333-565-22
; Sequence 22, Application US/08333565
; Patent No. 5622852
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,565
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
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; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-333-565-22

Query Match
Best Local Similarity 30.9%; Score 30; DB 1; Length 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 11 PYTAPG 16
Db 3 PYLAPG 8

RESULT 5
US-08-661-479-22
; Sequence 22, Application US/08661479
; Patent No. 5834209
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,479
; FILING DATE: 11-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,565
; FILING DATE: 31-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-661-479-22

Query Match
Best Local Similarity 83.3%; Score 30; DB 1; Length 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

OY 11 PYTARG 16  
Db 3 PYLARG 8  
RESULT 6  
US-09-042-353-366  
Sequence 366, Application US/09042353  
Patent No. 6255458  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for  
Producing Heterologous Antibodies  
TITLE OF INVENTION: Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 421  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/042,353  
FILING DATE: 13-MAR-1996  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/810,279  
FILING DATE: 17-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/853,408  
FILING DATE: 18-MAR-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/904,068  
FILING DATE: 23-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/096,762  
FILING DATE: 22-JUL-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 10-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/209,741  
FILING DATE: 09-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/352,322  
FILING DATE: 07-DEC-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/544,404  
FILING DATE: 10-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/728,463  
FILING DATE: 10-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US96/16433  
FILING DATE: 10-OCT-1996

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/758,417  
FILING DATE: 02-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO PCT/US97/21803  
FILING DATE: 01-DEC-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Apple, Randolph T.  
REGISTRATION NUMBER: 36,429  
REFERENCE/DOCKET NUMBER: 014643-009040US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 366:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-042-353-366  
Query Match 29.9%; Score 29; DB 2; Length 9;  
Best Local Similarity 83.3%; Pred. No. 5e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0;  
Gaps 0;  
OY 8 NIPYPT 13  
Db 4 NSFPT 9  
RESULT 7  
US-08-758-417A-214  
Sequence 214, Application US/08758417A  
Patent No. 6300129  
GENERAL INFORMATION:  
APPLICANT: Lonberg, Nils  
APPLICANT: Kay, Robert M.  
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for  
Producing Heterologous Antibodies  
NUMBER OF SEQUENCES: 417  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/758,417A  
FILING DATE: 02-DEC-1996  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/728,463  
FILING DATE: 10-OCT-1996  
APPLICATION NUMBER: US 08/544,404  
FILING DATE: 10-OCT-1995  
APPLICATION NUMBER: US 08/352,322  
FILING DATE: 07-DEC-1994  
APPLICATION NUMBER: US 08/209,741  
FILING DATE: 09-MAR-1994  
APPLICATION NUMBER: US 08/165,699  
FILING DATE: 10-DEC-1993  
APPLICATION NUMBER: US 08/161,739  
FILING DATE: 03-DEC-1993  
APPLICATION NUMBER: US 08/155,301  
FILING DATE: 18-NOV-1993  
APPLICATION NUMBER: US 08/096,762

FILED DATE: 22-JUL-1993  
APPLICATION NUMBER: US 08/053,131  
FILING DATE: 26-APR-1993  
APPLICATION NUMBER: US 07/990,860  
FILING DATE: 16-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Serafini, Andrew T.  
REGISTRATION NUMBER: 41,303  
REFERENCE/DOCKET NUMBER: 014643-009030US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0300  
TELEFAX: (415) 576-0200  
INFORMATION FOR SEQ ID NO: 214:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 214:  
US-08-758-417A-214

Query Match 29.9%; Score 29; DB 2; Length 9;  
Best Local Similarity 83.3%; Pred. No. 5e+05;  
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 NIPFYT 13  
Db 4 NSFPHY 9

RESULT 8  
US-09-307-265A-14  
Sequence 14, Application US/09307265A  
Patent No. 6225456  
GENERAL INFORMATION:  
APPLICANT: Gu, Trent  
APPLICANT: Orlita, Satoshi  
TITLE OF INVENTION: RAS SUPPRESSOR SUR-5  
FILE REFERENCE: UTC-03732  
CURRENT APPLICATION NUMBER: US/09/307,265A  
CURRENT FILING DATE: 1999-05-06  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 14  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Caenorhabditis elegans  
US-09-307-265A-14

Query Match 29.9%; Score 29; DB 2; Length 11;  
Best Local Similarity 62.5%; Pred. No. 2.6e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 11 PYTAGTK 18  
Db 1 PYTSGKK 8

RESULT 9  
US-08-278-774-20  
Sequence 20, Application US/08278774  
Patent No. 6653450  
GENERAL INFORMATION:  
APPLICANT: Berg, Richard A  
APPLICANT: Toman, David P  
APPLICANT: Wallace, Donald  
TITLE OF INVENTION: MUTATED RECOMBINANT COLLAGENS  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: COLLAGEN CORPORATION  
STREET: 2500 Faber Place

CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/278,774  
FILING DATE: 22-JUL-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rafayko, Kachi L  
REGISTRATION NUMBER: 36,644  
REFERENCE/DOCKET NUMBER: 94-018  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 354-4642  
TELEFAX: (415) 354-4752  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-278-774-20

Query Match 29.9%; Score 29; DB 2; Length 15;  
Best Local Similarity 41.7%; Pred. No. 3.6e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VDQKATNIPFY 12  
Db 2 IGGERKGGFAPY 13

RESULT 10  
US-09-526-195-9  
Sequence 9, Application US/09526195  
Patent No. 6699478  
GENERAL INFORMATION:  
APPLICANT: Hancock, Gerald E.  
APPLICANT: Tebbey, Paul W.  
TITLE OF INVENTION: ENHANCED IMMUNE RESPONSE TO ATTACHMENT  
FILE REFERENCE: 1646.1030-004  
CURRENT APPLICATION NUMBER: US/09/526,195  
CURRENT FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: US 60/084,863  
PRIOR FILING DATE: 1998-05-08  
PRIOR APPLICATION NUMBER: PCT/US98/19656  
PRIOR FILING DATE: 1998-09-17  
PRIOR APPLICATION NUMBER: US 60/059,684  
PRIOR FILING DATE: 1997-09-19  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Peptide  
US-09-526-195-9

Query Match 29.9%; Score 29; DB 2; Length 15;  
Best Local Similarity 50.0%; Pred. No. 3.6e+02;  
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 7 TNIPFYTAGTK 18



Db 1 TTILASTPGVK 12

## RESULT 11

US-08-957-130-19  
; Sequence 19, Application US/08957130  
; Patent No. 6280959  
; GENERAL INFORMATION:  
; APPLICANT: WO, Xue-Ru  
; APPLICANT: SUN, Tung-Tien  
; TITLE OF INVENTION: METHOD FOR SCREENING COMPOUNDS FOR  
; TITLE OF INVENTION: INHIBITING BACTERIAL ATTACHMENT TO HOST CELL RECEPTORS  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.  
; STREET: 419 Seventh Street N.W., Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/957,130  
; FILING DATE:  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: SUN=8  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 16 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-957-130-19

Query Match 29.9%; Score 29; DB 2; Length 16;

Best Local Similarity 50.0%; Pred. No. 3.8e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY 5 KATNIFPYTAPGK 18

Db 4 QVTNL----APGK 13

## RESULT 12

US-09-856-920-1  
; Sequence 1, Application US/09856920  
; Patent No. 6740325  
; GENERAL INFORMATION:  
; APPLICANT: Veda Research and Development Co.  
; TITLE OF INVENTION: Peptide-based vaccine for influenza  
; FILE REFERENCE: 9822 PCT  
; CURRENT APPLICATION NUMBER: US/09/856,920  
; CURRENT FILING DATE: 2002-02-19  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Influenza virus  
; US-09-856-920-1

Query Match 29.9%; Score 29; DB 2; Length 16;

Best Local Similarity 44.4%; Pred. No. 4.3e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 TNIPFYTAP 15

Db 5 SNCPYDVP 13

## RESULT 13

US-09-641-803-18  
; Sequence 18, Application US/09641803  
; Patent No. 6500798  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDGCH, Istvan  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND  
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS  
; FILE REFERENCE: 265,00220101  
; CURRENT APPLICATION NUMBER: US/09/641,803  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,310  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; US-09-641-803-18

Query Match 28.9%; Score 28; DB 2; Length 10;

Best Local Similarity 42.9%; Pred. No. 3.3e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 IFPYTAP 15

Db 1 VYPFTGP 7

## RESULT 14

US-09-641-802-18  
; Sequence 18, Application US/09641802  
; Patent No. 6852685  
; GENERAL INFORMATION:  
; APPLICANT: BOLDGCH, Istvan  
; TITLE OF INVENTION: TO PROMOTE NEURAL CELL DIFFERENTIATION  
; FILE REFERENCE: 265,00240101  
; CURRENT APPLICATION NUMBER: US/09/641,802  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,633  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; US-09-641-802-18

Query Match 28.9%; Score 28; DB 2; Length 10;

Best Local Similarity 42.9%; Pred. No. 3.3e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 IFPYTAP 15

Db 1 VYPFTGP 7

Db 1 VYPFTGP 7

RESULT 15  
US-09-641-801-18  
; Sequence 18, Application US/09641801  
; Patent No. 6903068  
; GENERAL INFORMATION:  
; APPLICANT: STANTON, G. John  
; APPLICANT: HUGHES, Thomas K.  
; APPLICANT: BOLDOGH, Istvan  
; APPLICANT: GEORGIADIS, Jerzy  
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOG  
; TITLE OF INVENTION: THEREOF  
; TITLE OF INVENTION: FOR INDUCING CYTOKINES  
; FILE REFERENCE: 265.00230101  
; CURRENT APPLICATION NUMBER: US/09/641,801  
; CURRENT FILING DATE: 2000-08-17  
; PRIOR APPLICATION NUMBER: 60/149,311  
; PRIOR FILING DATE: 1999-08-17  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: peptide  
US-09-641-801-18

Query Match 28.9%; Score 28; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 3.3e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 9 IFPYTAP 15  
:::|  
Db 1 VYPFTGP 7

Search completed: May 30, 2006, 15:09:25  
Job time : 20.3333 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2006, 15:04:28 ; Search time 12 Seconds  
(without alignments)  
144.325 Million cell updates/sec

Title: US-10-758-165A-9

Perfect score: 97  
Sequence: 1 VDGKATNIFPYTAPGK 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 263416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28.9	15	2	I53284	T-cell receptor be
2	27.8	15	2	PA0099	phenotypic variati
3	27.8	17	2	H49048	T-cell receptor be
4	27.8	18	2	A59137	protein P11 - gold
5	26.8	18	2	A61577	24k serine protein
6	25.8	15	2	D28587	T-cell receptor be
7	25.8	15	2	F28587	T-cell receptor be
8	25.8	16	2	B28587	T-cell receptor be
9	25.8	16	2	F53284	T-cell receptor be
10	24.7	14	2	B58502	36k kidney stone p
11	24.7	15	2	PH1318	ig heavy chain DJ
12	24.7	17	2	S18534	hypothetical prote
13	24.7	18	2	A25941	ig heavy chain J-H
14	23.7	12	2	C20907	ig kappa-1 chain J
15	23.7	13	2	S23640	ig kappa chain J s
16	23.7	13	2	C53275	ig kappa-1 chain J
17	23.7	15	2	B45115	peptidylprolyl iso
18	23.7	16	2	S03532	ig heavy chain J r
19	23.7	16	2	PS0383	ig heavy chain J r
20	23.7	16	2	S38292	30k allergen - rye
21	23.7	18	2	PQ0072	T-cell receptor be
22	23.7	18	2	S20322	gluten - wheat
23	23.7	18	2	C50786	urinary tract ston
24	22.7	12	2	PQ0786	NADH2 dehydrogenas
25	22.7	13	2	S01904	H--transporting tw
26	22.7	14	2	PH1306	ig heavy chain DJ
27	22.7	15	2	PA0056	protein QP200002 -
28	22.7	15	2	PA0087	cytochrome c2 - fu
29	22.7	17	2	C84063	hypothetical prote

30	21	21.6	10	2	S71948	matrix metalloprot
31	21	21.6	10	2	A39745	endo-glucosylceram
32	21	21.6	12	2	A53524	ubiquinol-cytochro
33	21	21.6	14	2	PL0142	carbon-monoxide de
34	21	21.6	14	2	S59495	formate dehydrogen
35	21	21.6	15	2	B61457	alpha-glucosidase
36	21	21.6	15	2	S36893	ribosomal protein
37	21	21.6	16	2	E53284	T-cell receptor be
38	21	21.6	17	2	S50901	chlorophyll a/b-di
39	21	21.6	18	2	S57518	T cell receptor be
40	21	21.6	18	2	S70612	alpha-macroglobuli
41	20	20.6	9	2	D48186	ATPase RI subunit
42	20	20.6	9	2	S10784	enamelin i - bovin
43	20	20.6	13	2	B58533	CD61 homolog - cha
44	20	20.6	14	2	S22236	lipoxigenase (EC 1
45	20	20.6	14	2	G44957	photosystem II oxy

## ALIGNMENTS

RESULT 1  
I53284  
T-cell receptor beta 2 chain J region, Jbeta2.7 - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C:Date: 02-May-1994 #sequence #revision 18-Nov-1994 #text\_change 05-Nov-1999  
C:Accession: I53284  
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.  
Mol. Immunol. 28, 881-888, 1991  
A:Title: Evolutionarily conserved organization and sequences of germline diversity and  
A:Reference number: A53284; MUID:91342695; PMID:1678859  
A:Accession: I53284  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-15 <HAR>  
A:Cross-references: UNIPARC:UPI0000115418; GB:S60737; NID:G233916; PIDN:AAB19525.1; PID  
A>Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIPI:60747)  
C:Keywords: T-cell receptor

Query Match 28.9%; Score 28; DB 2; Length 15;  
Best Local Similarity 71.4%; Pred. NO. 2.1e+02;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 YTAGTK 18  
DB 5 YFGGK 11

RESULT 2  
PA0099  
Phenotypic variation protein - fungus (Fusarium sporotrichioides) (fragment)  
C:Species: Fusarium sporotrichioides  
C:Date: 20-Feb-1995 #sequence #revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: PA0099  
R:Chow, L.P.; Fukaya, N.; Sugiyama, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.  
submitted to JIPD, October 1994  
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotric  
A:Reference number: PA0051  
A:Accession: PA0099  
A:Molecule type: protein  
A:Residues: 1-15 <CHO>  
A:Cross-references: UNIPROT:Q7M4Y7; UNIPARC:UPI0000178405

Query Match 27.8%; Score 27; DB 2; Length 15;  
Best Local Similarity 62.5%; Pred. NO. 3.2e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 FPYTAGT 17  
DB 7 FKYSASGT 14

RESULT 3

H49048  
T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 30-May-1997  
C/Accession: H49048  
R/Sjoud, M.; Kjelsgaard-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.  
Eur. J. Immunol. 22, 2413-2416, 1992  
A/Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenile  
A/Reference number: A49048; MUID:92387250; PMID:11387614  
A/Accession: H49048  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-17 <STO>  
A/Cross-references: UNIPARC:UPI0000176DF0  
A/Experimental source: patient SS, IL-2R+ synovial T-cells  
A/Note: sequence extracted from NCBI backbone (NCBI:113270)  
C/Suprafamily: immunoglobulin V region; immunoglobulin homology  
C/Keywords: T-cell receptor

Query Match 27.8%; Score 27; DB 2; Length 17;  
Best Local Similarity 62.5%; Pred. No. 3.6e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ATNIFPYT 13  
| | | | |  
DB 8 AWTFFPYT 15

#### RESULT 4

A59137  
protein p11 - golden needle mushroom (fragment)  
C/Species: Flammulina velutipes (golden needle mushroom)  
C/Date: 12-Nov-1999 #sequence\_revision 12-Nov-1999 #text\_change 09-Jul-2004  
C/Accession: A59137  
R/Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.  
A/Title: Differences of proteins expressed in the fruiting dikaryon and the non-fr  
A/Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr  
A/Reference number: A59137  
A/Accession: A59137  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-18 <SAK>  
A/Cross-references: UNIPROT:Q7M4W6; UNIPARC:UPI000017CB27

Query Match 27.8%; Score 27; DB 2; Length 18;  
Best Local Similarity 80.0%; Pred. No. 3.9e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 PYTAP 15  
| | | | |  
DB 2 PYTSP 6

#### RESULT 5

A61577  
24k serine proteinase (BC 3.4.21.-) - Streptomyces fradiae (fragment)  
C/Species: Streptomyces fradiae  
C/Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004  
C/Accession: A61577  
R/Sinha, U.; Wolz, S.A.; Lad, P.J.  
Int. J. Biochem. 23, 979-984, 1991  
A/Title: Two new extracellular serine proteases from Streptomyces fradiae.  
A/Reference number: A61577; MUID:92155439; PMID:1766859  
A/Accession: A61577  
A/Molecule type: protein  
A/Residues: 1-18 <SIN>  
A/Cross-references: UNIPROT:Q7M198; UNIPARC:UPI000017AE13  
C/Keywords: extracellular protein; hydrolase; serine proteinase

Query Match 26.8%; Score 26; DB 2; Length 18;  
Best Local Similarity 41.7%; Pred. No. 5.7e+02;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGKATNIFPY 12  
| | | | |  
DB 2 VGGTRAAQGFPPW 13

#### RESULT 6

D28587  
T-cell receptor beta-2 chain J-B2.5 segment - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999  
C/Accession: D28587  
R/Toyonaga, B.; Yoshikaki, Y.; Vadasz, V.; Chin, B.; Mak, T.W.  
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
A/Title: Organization and sequences of the diversity, joining, and constant region gene  
A/Reference number: A94081; MUID:86094276; PMID:3866244  
A/Accession: D28587  
A/Molecule type: DNA  
A/Residues: 1-15 <TOY>  
A/Cross-references: UNIPARC:UPI0000113C7C; GB:M14159; NID:g338852; PIDN:AAA60679.1; PID  
C/Keywords: T-cell receptor

Query Match 25.8%; Score 25; DB 2; Length 15;  
Best Local Similarity 57.1%; Pred. No. 6.9e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 YTAGTK 18  
| | | | |  
DB 5 YFGPGTR 11

#### RESULT 7

F28587  
T-cell receptor beta-2 chain J-B2.7 segment - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999  
C/Accession: F28587  
R/Toyonaga, B.; Yoshikaki, Y.; Vadasz, V.; Chin, B.; Mak, T.W.  
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
A/Title: Organization and sequences of the diversity, joining, and constant region gene  
A/Reference number: A94081; MUID:86094276; PMID:3866244  
A/Accession: F28587  
A/Molecule type: DNA  
A/Residues: 1-15 <TOY>  
A/Cross-references: UNIPARC:UPI0000113C7E; GB:M14159; NID:g338852; PIDN:AAA60681.1; PID  
C/Keywords: T-cell receptor

Query Match 25.8%; Score 25; DB 2; Length 15;  
Best Local Similarity 57.1%; Pred. No. 6.9e+02;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 YTAGTK 18  
| | | | |  
DB 5 YFGPGTR 11

#### RESULT 8

B28587  
T-cell receptor beta-2 chain J-B2.3 segment - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 05-Nov-1999  
C/Accession: B28587  
R/Toyonaga, B.; Yoshikaki, Y.; Vadasz, V.; Chin, B.; Mak, T.W.  
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985  
A/Title: Organization and sequences of the diversity, joining, and constant region gene  
A/Reference number: A94081; MUID:86094276; PMID:3866244  
A/Accession: B28587  
A/Molecule type: DNA  
A/Residues: 1-16 <TOY>  
A/Cross-references: UNIPARC:UPI000002FDD6; GB:M14159; NID:g338852; PIDN:AAA60677.1; PID  
C/Keywords: T-cell receptor

Query Match 25.8%; Score 25; DB 2; Length 16;  
Best Local Similarity 57.1%; Pred. No. 7.4e+02;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 YTPAGTK 18  
| | | |  
| | | |

Db 6 YFGPGTR 12

## RESULT 9

F53284

T-cell receptor beta 2 chain J region, Jbeta2.3 - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999

C/Accession: F53284

R:Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A/Title: Evolutionarily conserved organization and sequences of germline diversity and J

A/Reference number: A53284; MUID:91342695; PMID:1678859

A/Accession: F53284

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-16 <HNR>

A/Cross-references: UNIPARC:UPI0000115415; GB:S60737; NID:g233916; PIDN:AA19522.1; PID:

A/Note: sequence extracted from NCBI backbone (NCBI:60737, NCBI:60744)

C/Keywords: T-cell receptor

Query Match 25.8%; Score 25; DB 2; Length 16;

Best Local Similarity 57.1%; Pred. No. 7.4e+02;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 YTPAGTK 18  
| | | |  
| | | |

Db 6 YFGPGTR 12

## RESULT 10

B58502

36k kidney stone protein - unidentified bacterium (fragment)

C/Species: unidentified bacterium

C/Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 10-Jul-1998

C/Accession: B58502

R:Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A/Description: The proteins of kidney and gallbladder stones.

A/Reference number: A58501

A/Accession: B58502

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-14 <BIN>

A/Cross-references: UNIPARC:UPI000017A8D0

A/Note: tentative identification of 8-Tyr and 9-Trp

Query Match 24.7%; Score 24; DB 2; Length 14;

Best Local Similarity 66.7%; Pred. No. 9.5e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 NIFPYT 13  
| | | |  
| | | |

Db 4 NLFGYT 9

## RESULT 11

PH1318

Ig heavy chain DJ region (clone C527-121) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C/Accession: PH1318

R:Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A/Reference number: PH1302; MUID:93094761; PMID:1460419

A/Accession: PH1318

A/Molecule type: DNA

A/Residues: 1-15 <MAS>

A/Cross-references: UNIPARC:UPI000017C244

C/Keywords: heterotetramer; Immunoglobulin

Query Match 24.7%; Score 24; DB 2; Length 15;

Best Local Similarity 45.5%; Pred. No. 1e+03;

Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 7 TNIFPYTAPGT 17  
| | | | |  
| | | | |

Db 5 TGYFDWVGQGT 15

## RESULT 12

S18534

hypothetical protein 7 (eryG 3' region) - Saccharopolyspora erythraea (fragment)

C/Species: Saccharopolyspora erythraea

C/Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 07-Apr-1994

C/Accession: S18534

R:Haydock, S.F.; Dowson, J.A.; Dillon, N.; Roberts, G.A.; Cortes, J.; Leadlay, P.F.

Mol. Gen. Genet. 230, 120-128, 1991

A/Title: Cloning and sequence analysis of genes involved in erythromycin biosynthesis 1

methylintraseferases.

A/Reference number: S18530; MUID:92079886; PMID:1840640

A/Accession: S18534

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-17 <HMY>

A/Cross-references: UNIPARC:UPI000017AD81; EMBL:X60379

A/Note: the authors translated the codon CTG for residue 12 as Gly

Query Match 24.7%; Score 24; DB 2; Length 17;

Best Local Similarity 62.5%; Pred. No. 1.2e+03;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 IFPYTAPG 16  
| | | | |  
| | | | |

Db 1 IFPAVASG 8

## RESULT 13

A25941

Ig heavy chain J-H1 region - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 05-Jun-1988 #sequence\_revision 05-Jun-1988 #text\_change 23-Jul-1999

C/Accession: A25941; JH0666

R:Bruggemann, M.; Frey, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.

Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986

A/Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibo

A/Reference number: A25941; MUID:86287397; PMID:3016742

A/Accession: A25941

A/Molecule type: DNA

A/Residues: 1-18 <BRU>

A/Cross-references: UNIPARC:UPI0000114C27; db:M13798; NID:g204707; PIDN:AAA1371.1; PID

R:Lang, P.; Mociat, R.

Gene 102, 261-264, 1991

A/Title: Immunoglobulin heavy-chain joining genes in the rat: comparison with mouse and

A/Reference number: JH0666; MUID:91340162; PMID:1908401

A/Accession: JH0666

A/Molecule type: DNA

A/Residues: 1-18 <LAN>

A/Cross-references: UNIPARC:UPI0000114C27; EMBL:X56791

C/Superfamily: Immunoglobulin V region; Immunoglobulin homology

C/Keywords: heterotetramer; Immunoglobulin

Query Match 24.7%; Score 24; DB 2; Length 18;

Best Local Similarity 50.0%; Pred. No. 1.3e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 FPYTAPGT 17  
| | | | |  
| | | | |

Db 5 FDFWGPQT 12

## RESULT 14

C20907  
IG kappa-1 chain J3 region - rabbit  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 10-Aug-1990 #sequence\_revision 10-Aug-1990 #text\_change 16-Aug-1996  
C/Accession: C20907  
R:Emorine, L.; Max, E.E.  
Nucleic Acids Res. 11, 8877-8890, 1983  
A/Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multiple  
A/Reference number: A20907; MUID:84169523; PMID:6324107  
A/Accession: C20907  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-12 <EMO>  
A/Cross-references: UNIPARC:UPI000017C5CF  
C/Keywords: heterotetramer; immunoglobulin

## Query Match

Best Local Similarity 23.7%; Score 23; DB 2; Length 12;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PGTK 18  
|||||

DB 5 PGTK 8

## RESULT 15

S23640  
IG kappa chain J segment (J-kappa-3) - human  
C/Species: Homo sapiens (man)  
C/Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Aug-1996  
C/Accession: S23640  
R:Huber, C.; Klobeck, H.G.; Zachau, H.G.  
Eur. J. Immunol. 22, 1561-1565, 1992  
A/Title: Ongoing V(kappa)-J(kappa) recombination after formation of a productive V(kappa)  
A/Reference number: S23637; MUID:92289816; PMID:1601042  
A/Accession: S23640  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-13 <HUB>  
A/Cross-references: UNIPARC:UPI0000116784; EMBL:X63370  
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991  
C/Keywords: heterotetramer; immunoglobulin

## Query Match

Best Local Similarity 23.7%; Score 23; DB 2; Length 13;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PGTK 18  
|||||

DB 5 PGTK 8

Search completed: May 30, 2006, 15:08:21  
Job time : 13 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2006, 15:01:11 ; Search time 68.6667 Seconds  
(without alignments)  
242.480 Million cell updates/sec

Title: US-10-758-165A-9

Perfect score: 97  
Sequence: 1 VDCQKATNIFPYTAPGTX 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 12648

Minimum DB seq length: 0  
Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: UniProt 7.2:\*  
1: uniprot\_sprot:\*  
2: uniprot\_tramb1:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	35.1	17	2	046473_FELCA
2	32	33.0	8	2	Q70Y88_PLAMT
3	28.5	29.4	18	2	Q9TWM4_LUCCU
4	28	28.9	16	2	Q3ZEV4_9CHAR
5	27.5	28.4	16	2	Q8LIY7_PLEBO
6	27	27.8	15	2	Q7M4Y7_FUSSP
7	27	27.8	16	2	Q3ZEV6_9CHAR
8	27	27.8	18	2	Q7M4W6_FLAYE
9	27	27.8	18	2	Q3TW38_MOUSE
10	26	26.8	15	1	CWP16_LYCES
11	26	26.8	15	2	Q7S007_NEUCR
12	26	26.8	18	2	Q7M198_STRFR
13	25	25.8	15	2	Q9UR63_EMENT
14	24	24.7	14	2	Q714T5_SCRYP
15	24	24.7	15	2	Q69142_STRPY
16	24	24.7	16	2	Q3ZEV7_9CHAR
17	24	24.7	17	2	Q65Y26_HORSE
18	23	23.7	8	2	Q5ZEV7_HUMAN
19	23	23.7	10	2	Q9ZIB1_CLOPI
20	23	23.7	14	1	CWP27_TOBAC
21	23	23.7	14	2	P78359_HUMAN
22	23	23.7	15	2	Q5D4R7_9CYAN
23	23	23.7	15	2	Q85HM7_MOTFL
24	23	23.7	16	2	Q7M263_SECCF
25	23	23.7	16	2	Q8LIY8_9CYAN
26	23	23.7	16	2	Q89560_HNV8
27	23	23.7	16	2	Q3ZEV7_9CHAR
28	23	23.7	16	2	Q3ZEV2_9CHAR
29	23	23.7	16	2	Q3ZEW8_9CHAR
30	23	23.7	16	2	Q3ZEX1_9CHAR
31	23	23.7	16	2	Q3ZEV3_9CHAR

32	23	23.7	16	2	Q3ZEV9_9CHAR	Q3ZEV9_tringa eryt
33	23	23.7	16	2	Q3ZEV5_9CHAR	Q3ZEV5_catopropho
34	23	23.7	16	2	Q5R3U1_XENLA	Q5R3U1_xenopus lae
35	23	23.7	17	2	Q9PRU8_CHICK	Q9PRU8_gallus gall
36	23	23.7	18	2	Q7M4Q7_HUMAN	Q7M4Q7_homo sapien
37	23	23.7	18	2	Q7M1G0_WHEAT	Q7M1G0_triticum ae
38	22	22.7	8	2	Q59AR6_HUMAN	Q59AR6_homo sapien
39	22	22.7	10	2	Q71VW2_MOUSE	Q71VW2_mus musculu
40	22	22.7	11	1	PVK1_PERYR	P4657_perisphaeti
41	22	22.7	12	2	Q7M2G3_VICFA	Q7M2G3_vicia faba
42	22	22.7	14	2	Q70Y94_OCIUM	Q70Y94_ocimum grat
43	22	22.7	15	2	Q7M4Z7_FUSSP	Q7M4Z7_fusarium sp
44	22	22.7	15	2	Q9TRR5_BOVIN	Q9TRR5_bos taurus
45	22	22.7	15	2	Q9TRR8_PIG	Q9TRR8_sus scrofa

## ALIGNMENTS

RESULT 1	046473_FELCA	PRELIMINARY; PRT; 17 AA.
ID	046473_FELCA	PRELIMINARY; PRT; 17 AA.
AC	046473;	
DT	01-JUN-1998,	integrated into UniProtKB/TrEMBL.
DT	01-JUN-1998,	sequence version 1.
DT	07-FEB-2006,	entry version 18.
DE	Lactase dehydrogenase A (Fragment).	
GN	Name=LDHA;	
OS	Felis silvestris catus (Cat).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;	
OC	Felinae; Felis;	
OX	NCBI_TaxID=9685;	
RN	[1]	
RP	NUCLEOTIDE SEQUENCE.	
RC	STRAIN=domesticus;	
RX	MEDLINE=97141918; PubMed=8988168;	
RA	Lyons L.A., Laughlin T.F., Copeland N.G., Jenkins N.A., Womack J.E.,	
RA	O'Brien S.J.;	
RT	"Comparative anchor tagged sequences (CATS) for integrative mapping of	
RT	mammalian genomes.";	
RL	Nat. Genet. 15:47-56(1997).	
CC	Copyrighted by the UniProt Consortium, see <a href="http://www.uniprot.org/terms">http://www.uniprot.org/terms</a>	
CC	Distributed under the Creative Commons Attribution-NonDerivs license	
CC	EMBL; AF012095; AAC00072.2; -; Genomic_DNA.	
DR	EMBL; AF012095; AAC00072.2; -; Genomic_DNA.	
FT	NON_TER	1
FT	NON_TER	17
SQ	SEQUENCE	17 AA; 2018 MW; E47943B2E187C1FC CRC64;
QY	Query Match	35.1%; Score 34; DB 2; Length 17;
QY	Best Local Similarity	46.2%; Pred. No. 2.9e+02;
Db	Matches	6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Db	3 GQKATNIFPYTAP 15	
Db	3 GQKATNIFPYTAP 15	
RESULT 2	Q70Y88_PLAMT	PRELIMINARY; PRT; 8 AA.
ID	Q70Y88_PLAMT	PRELIMINARY; PRT; 8 AA.
AC	Q70Y88;	
DT	05-JUL-2004,	integrated into UniProtKB/TrEMBL.
DT	05-JUL-2004,	sequence version 1.
DT	07-FEB-2006,	entry version 8.
DE	Ribosomal protein (Fragment).	
GN	Name=Ips16;	
OS	Platostoma fimbriatum.	
OG	Plastid.	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;	

```

OC asteride; lamids; lamiales; Lamnaceae; Nepetoideae; Ocimeae;
OC Placostoma.
OX NCBI_TaxID=204168;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;
RA Paton A., Springate D.A., Stude S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.,
RT "Phylogeny and evolution of basilis and allies (Ocimeae, Labiatae)
RT based on three plastid DNA regions."
RL Mol. Phylogenet. Evol. 31:277-299(2004).
CC -----
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CC
CC EMBL; A505568; CAD5489.1; -; Genomic_DNA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
KM Ribosomal protein.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 789 MW; 86786772D1B84772 CRC64;

Query Match 33.0%; Score 32; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAPG 16
   |||
   |||
Db 2 PYTVPG 7

RESULT 3
Q9TWL4_LUCCU PRELIMINARY; PRT; 18 AA.
ID Q9TWL4_LUCCU
AC Q9TWL4;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE 25 kDa chymotrypsin-like enzyme (Fragment).
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Lucilia.
OX NCBI_TaxID=7375;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95219141; PubMed=7704304;
RA Casu R.E., Pearson R.D., Jarney J.M., Cadogan L.C., Riding G.A.,
RA Tellam R.L.;
RT "Excretory/secretory chymotrypsin from Lucilia cuprina: purification,
RT enzymatic specificity and amino acid sequence deduced from mRNA."
RL Insect Mol. Biol. 3:201-211(1994).
CC -----
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CC
CC SEQUENCE 18 AA; 1922 MW; 352EB0729B126B11 CRC64;

Query Match 29.4%; Score 28.5; DB 2; Length 18;
Best Local Similarity 58.3%; Pred. No. 2.5e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 2 DGQKAT-NIPY 12
   :|||
   :|||
Db 3 NQGEATVQGFY 14

RESULT 4
Q3ZEV4_9CHAR PRELIMINARY; PRT; 16 AA.
ID Q3ZEV4_9CHAR
AC Q3ZEV4;
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.

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DT 07-FEB-2006, entry version 3.
DE ATP synthase F0 subunit 8 (Fragment).
GN Name=ATP8;
OS Tringa totanus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinoptera; Aves; Neognathae; Charadriiformes; Scolopacidae; Tringa.
OX NCBI_TaxID=171271;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pereira S.L., Baker A.J.;
RT "Multiple gene evidence for parallel evolution and retention of
RT ancestral morphological states in the shanks (Charadriiformes;
RT Scolopacidae)."
RL Condor 107:514-526(2005).
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CC
CC EMBL; AY894271; AAX94014.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KM Mitochondrion.
FT NON_TER 1 1
FT NON_TER 1655 MW; 75D680373ACCF82D CRC64;
SQ SEQUENCE 16 AA; 1965 MW; 75D680373ACCF82D CRC64;

Query Match 28.9%; Score 28; DB 2; Length 16;
Best Local Similarity 54.5%; Pred. No. 2.7e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 TNIPYTPAGT 17
   |||
   |||
Db 6 TKITPWTWPWT 16

RESULT 5
Q8LIY7_PLEBO PRELIMINARY; PRT; 16 AA.
ID Q8LIY7_PLEBO
AC Q8LIY7;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Proteolysis-inducing tag (Fragment).
OC Plectonema boryanum.
OC Bacteria; Cyanobacteria; Oscillatoriales; Lepolyngya.
OX NCBI_TaxID=1184;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=UTEX 485;
RX MEDLINE=21970088; PubMed=11972342; DOI=10.1093/nar/30.9.2025;
RA Williams K.P.;
RT "Descent of a split RNA."
RL Nucleic Acids Res. 30:2025-2030(2002).
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CC
CC EMBL; AY082652; AAM03311.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 1640 MW; 60FE5985B9B00982 CRC64;
SQ SEQUENCE 16 AA; 1640 MW; 60FE5985B9B00982 CRC64;

Query Match 28.4%; Score 27.5; DB 2; Length 16;
Best Local Similarity 53.8%; Pred. No. 3.3e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 6 ATNIFPY---TAP 15
   |||
   |||
Db 1 ANNIVPAPKRTAP 13

RESULT 6
Q7M4Y7_FUSSP PRELIMINARY; PRT; 15 AA.
ID Q7M4Y7_FUSSP
AC Q7M4Y7;

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DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Phenotypic variation protein (Fragment).
OS Fusarium sporotrichioides.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OC NCBI_TaxID=5514;
RN [1]
RP PROTEIN SEQUENCE.
RA Chow L.P., Fukaya N., Sugiyura Y., Ueno Y., Tabuchi K., Tsubota A.;
RA Submitted (OCT-1994) to the PIR data bank.
RL
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CC -----
DR PIR, PA0099; PA0099.
FT NON_TER 1 15
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1648 MW; 4C4FAFA966995807 CRC64;

Query Match
Best Local Similarity 27.8%; Score 27; DB 2; Length 15;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 PPTAPGT 17
DB 7 FRTSASGT 14

RESULT 7
Q3ZEY6_9CHAR PRELIMINARY; PRT; 16 AA.
ID Q3ZEY6_9CHAR
AC Q3ZEY6_9CHAR
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE ATP synthase F0 subunit 8 (Fragment).
GN Name=ATP8;
OS Tringa flavipes.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Aves; Neognathae; Charadriiformes; Scolopacidae; Tringa.
OC NCBI_TaxID=161739;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pereira S.L., Baker A.J.;
RT "Multiple gene evidence for parallel evolution and retention of
RT ancestral morphological states in the shanks (Charadriiformes:
RT Scolopacidae).";
RL Condor 107:514-526(2005).
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CC -----
DR EMBL: AY894261; AAX93984.1; -; Genomic_DNA.
DR GO: GO:0005739; C:mitochondrion; IEA.
KM Mitochondrion.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1893 MW; 6FF802724F1F82D CRC64;

Query Match
Best Local Similarity 27.8%; Score 27; DB 2; Length 16;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 6 ATNIPYTPAGT 17
DB 5 ATKTTPTWTPWT 16

RESULT 8
Q7M4W6_FLAVE PRELIMINARY; PRT; 18 AA.
ID Q7M4W6_FLAVE

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AC Q7M4W6;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Protein Pil (Fragment).
OS Flammulina velutipes.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Tricholomataceae; Flammulina.
OC NCBI_TaxID=38945;
RN [1]
RP PROTEIN SEQUENCE.
RA Sakamoto Y., Ando A., Tamai Y., Miura K.;
RA Submitted (NOV-1999) to the PIR data bank.
RL
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CC -----
DR PIR, A59137; A59137.
FT NON_TER 1 18
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1956 MW; FE0434B0AF005AEC CRC64;

Query Match
Best Local Similarity 27.8%; Score 27; DB 2; Length 18;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 PYTAP 15
DB 2 PYTSP 6

RESULT 9
Q3TW38_MOUSE PRELIMINARY; PRT; 18 AA.
ID Q3TW38_MOUSE
AC Q3TW38_MOUSE
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Osteoclast-like cell CDNA, RIKEN full-length enriched library,
DE clone:1420034D23 product:RNA binding motif, single stranded
DE interacting protein 1, full insert sequence. (Fragment).
GN Name=Rbm61;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J;
RC PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.U., Wilming L.G., Aldins E., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Attalini R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgakilas P., Gingeras T.R., Gojovic T., Green R.E.,
RA Gustincich S., Harbers M., Hayashizaki Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,

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RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
RA Liuni S., McMilliam S., Madan Babu M., Madera M., Marchionni L.,  
RA Matcunda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
RA Motegut-Tabar S., Mulder N., Nakano N., Nakuchi H., Ng P.,  
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,  
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Seno S., Seesla L., Sheng Y.,  
RA Schombach C., Sekiguchi K., Sempé C.A., Seno S., Sinclair B., Taki K.,  
RA Shibata K., Shimada K., Silva D., Takenaka Y., Taki K.,  
RA Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Teichmann S.A.,  
RA Tamajo K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K.,  
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide M., Bult C.,  
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
RA Wahlstedt C., Maticic K., Katayama M., Suzuki M., Aoki J., Arakawa T.,  
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
RA Iida J., Imanura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niimiyu N.,  
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,  
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
RA Hayashizaki Y.,  
RA "the transcriptional landscape of the mammalian genome";  
RA Science 309:1559-1563(2005).  
[3]  
RA NUCLEOTIDE SEQUENCE.  
RA STRAIN=C57BL/6J;  
RA PubMed=16141073; DOI=10.1126/science.1112009;  
RA RIKEN Genome Exploration Research Group, and Genome Science Group  
RA (Genome Network Core Team) and the FANTOM Consortium;  
RA "Anticancer transcription in the mammalian Transcriptionome";  
RA Science 309:1564-1566(2005).  
[4]  
RA NUCLEOTIDE SEQUENCE.  
RA STRAIN=C57BL/6J;  
RA MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Nikaido I., Oseato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schombach J.,  
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schirml L.M., Kanepin A., Matsuda H., Batalov S., Betsel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Guentrich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawagawa Y., Kedzierski R.W., King B.L.,  
RA Konegaya A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sanderlin A., Schneider C., Sempé C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Welis C.,  
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carlini P., Hayatsu N.,  
RA Hitozane-Tsukawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Sasaki D., Shingawa A.,  
RA Miyazaki A., Sakai K., Sasaki D., Shingawa A.,  
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RA "Analysis of the mouse transcriptome based on functional annotation of  
RA 60,770 full-length cDNAs";  
RA Nature 420:563-573(2002).  
[5]  
RA NUCLEOTIDE SEQUENCE.  
RA STRAIN=C57BL/6J;  
RA MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi I., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matcunda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kociwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schirml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carlini P., de Bonaldo M.F.,  
RA Blomstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Guentrich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima Y., Mazzarelli I., Sakamoto N.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schombach C., Seva T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
RA Hayashizaki Y.,  
RA "Functional annotation of a full-length mouse cDNA collection";  
RA Nature 409:685-690(2001).  
[6]  
RA NUCLEOTIDE SEQUENCE.  
RA STRAIN=C57BL/6J;  
RA MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carlini P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
RA "Normalization and subtraction of cap-trapper-selected cDNAs to  
RA prepare full-length cDNA libraries for rapid discovery of new genes";  
RA Genome Res. 10:1617-1630(2000).  
[7]  
RA NUCLEOTIDE SEQUENCE.  
RA STRAIN=C57BL/6J;  
RA MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carlini P.,  
RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
RA "RIKEN integrated sequence analysis (RISA) system-384-format  
RA sequencing pipeline with 384 multicapillary sequencer";  
RA Genome Res. 10:1757-1771(2000).  
[8]  
RA NUCLEOTIDE SEQUENCE.  
RA STRAIN=C57BL/6J;  
RA Arakawa T., Carlini P., Fukuda S., Hashizume W., Hayashida K.,  
RA Kawai J., Iida J., Imanura K., Imotani K., Itoh M., Kanagawa S.,  
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,  
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watahiki A.,  
RA Muramatsu M., Hayashizaki Y.,  
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
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CC  
CC EMBL: AK159851; BAB5428.1; -- mRNA.  
DR MGI: 1861774; RDMs1.  
DR GO: GO:0005634; C:nucleus; RCA.  
DR GO: GO:0003690; F:double-stranded DNA binding; RCA.  
DR GO: GO:0003722; F:RNA binding; RCA.  
DR GO: GO:0003697; F:single-stranded DNA binding; RCA.  
DR GO: GO:0006260; P:DNA replication; RCA.  
FT NON TER 1 1  
SQ SEQUENCE 18 AA; 2003 MW; 82F8AB5FD94EEA14 CRC64;

Query Match 27.8%; Score 27; DB 2; Length 18;  
Best Local Similarity 62.5%; Pred. No. 4.5e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
11 PYTAPGTX 18  
11 PYTFPKNK 18  
RESULT 10

CMP16 LYCES  
ID CMP16 LYCES STANDARD; PRT; 15 AA.  
AC P80812;  
DT 25-OCT-2005, integrated into UniProtKB/Swiss-Prot.  
DT 25-OCT-2005, sequence version 1.  
DT 07-FEB-2006, entry version 4.  
DE 40 kDa cell wall protein (Fragment).  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC Asterids; Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.  
OX NCBI\_TaxID=4081;  
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RP PROTEIN SEQUENCE, AND SUBCELLULAR LOCATION.  
RX MEDLINE=97332671; PubMed=9188482; DOI=10.1074/jbc.272.25.15841;  
RA Robertson D., Mitchell G.P., Gilroy J.S., Gerrish C., Bolwell G.P.,  
RA Slabas A.R.;  
RT "Differential extraction and protein sequencing reveals major  
RT differences in patterns of primary cell wall proteins from plants.";  
RL J. Biol. Chem. 272:15841-15848(1997).  
CC -1- SUBCELLULAR LOCATION: Cell wall.  
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CC Distributed under the Creative Commons Attribution-NonDerivs License  
CC  
CC  
CC Cell wall; Direct protein sequencing.  
FT CHAIN 1 >15 /FTid=PRO\_0000079677.  
FT NON\_TER 15 15  
SQ SEQUENCE 15 AA; 1705 MW; 1F328E5C82CA77BE CRC64;  
Query Match 26.8%; Score 26; DB 1; Length 15;  
Best Local Similarity 44.4%; Pred. No. 5.5e+03;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
Qy 10 PPTAPAGTK 18  
Db 6 PPTVQANR 14  
RESULT 11  
Q7S007 NEUCR PRELIMINARY; PRT; 15 AA.  
AC Q7S007;  
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.  
DT 15-DEC-2006, sequence version 1.  
DT 07-FEB-2006, entry version 8.  
DE Predicted protein.  
GN ORFNames=NCU09752.1;  
OS Neurospora crassa.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.  
OX NCBI\_TaxID=5141;  
[1]  
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].  
RC STRAIN=74-OR23-1A / FGSC 987;  
RX MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;  
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,  
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,  
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,  
RA Qui D., Tankelev P., Bell-Pedersen D., Nelson M.A.,  
RA Werner-Washburne M., Selitrenikoff C.P., Kinney J.A., Braun E.L.,  
RA Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,  
RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,  
RA Gauger-Tromann N., Barrett R., Gnerre S., Kamal M., Kamyssealis M.,  
RA Mauceli E., Bielek C., Rudd S., Fishman D., Kryzofova S.,  
RA Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S., Cogoni C.,  
RA Mactou G., Catchpole D.E.A., Li W., Pratt R.J., Omani S.A.,  
RA Desouza C.P.C., Glas N.L., Orbach M.J., Berglund J.A., Voelker R.,  
RA Yarden O., Plamann M., Selter S., Dunlap J.C., Radford A., Aramayo R.,  
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebdole D.J., Freitag M.,  
RA Paulsen I., Sachs M.S., Lander E.S., Nuebaum C., Birren B.W.;  
"The genome sequence of the filamentous fungus Neurospora crassa.";

RL Nature 422:859-868(2003).  
CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.  
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CC  
CC  
CC EMBL; AABX01000580; EAA28619.1; -; Genomic DNA.  
SQ SEQUENCE 15 AA; 1832 MW; 012D0180A8C7089D CRC64;  
Query Match 26.8%; Score 26; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 5.5e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 8 NIPPYT 13  
Db 2 NVFEXT 7  
RESULT 12  
Q7M198 STRPR PRELIMINARY; PRT; 18 AA.  
AC Q7M198;  
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.  
DT 15-DEC-2003, sequence version 1.  
DT 07-FEB-2006, entry version 7.  
DE 24k serine proteinase (EC 3.4.21.-) (Fragment).  
OS Streptomyces fradiae.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycinae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1906;  
[1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=92155439; PubMed=1786859; DOI=10.1016/0020-711X(91)90133-8;  
RA Sinha U., Wolz S.A., Lad P.J.;  
RT "Two new extracellular serine proteinases from Streptomyces fradiae.";  
RL Int. J. Biochem. 23:979-984(1991).  
CC  
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CC  
CC  
CC PIR: A61577; A61577. 1  
FT NON\_TER 1 1  
FT NON\_TER 18 18  
SQ SEQUENCE 18 AA; 2004 MW; 6D6DA167845934A5 CRC64;  
Query Match 26.8%; Score 26; DB 2; Length 18;  
Best Local Similarity 41.7%; Pred. No. 6.7e+03;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
Qy 1 VDGGKATNIPPY 12  
Db 2 VGGTRAAQEPFW 13  
RESULT 13  
Q9UR63 EMENI PRELIMINARY; PRT; 15 AA.  
AC Q9UR63;  
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
DT 01-MAY-2000, sequence version 1.  
DT 07-FEB-2006, entry version 11.  
DE Beta-D-FRUCTOFURANOSIDE FRUCTOHYDROLASE 60 kDa high molecular weight  
DE isoform (EC 3.2.1.26) (Fragment).  
OS Emericella nidulans (Aspergillus nidulans).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurotiiales; Trichocomaceae; Emericella.  
OX NCBI\_TaxID=162425;  
[1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=96409246; PubMed=8814228; DOI=10.1016/0167-4838(96)00073-8;  
RA Chen J.S., Saxton J., Hemming F.W., Peberdy J.F.;

```

RT      "Purification and partial characterization of the high and low
RT      molecular weight form (S- and F-form) of invertase secreted by
RT      Aspergillus nidulans."
RT      Blochim. Biophys. Acta 1296:207-218(1996).
RT      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs license
CC      -----
DR      GO:0004564; F:beta-fructofuranosidase activity; IEA.
SQ      SEQUENCE 15 AA; 1588 MW; 2C992B42211366BB CRC64;

Query Match      25.8%; Score 25; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 8.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      11 PYTAP 15
        |||
        10 PYTER 14

RESULT 14
Q714T5_9CRYP PRELIMINARY; PRT; 14 AA.
ID Q714T5_9CRYP
AC Q714T5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE tmRNA proteolysis tag (fragment).
DE Name=sstA;
OS Rhodomonas salina.
OC Plastid.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.
OX NCBI_TaxID=52970;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CCMP1319;
RX PubMed=14681369; DOI=10.1093/nar/gkh102;
RA Guenau de Nova P., Williams K.P.;
RT "The tmRNA website: reductive evolution of tmRNA in plastids and other
RT endosymbionts."
RL Nucleic Acids Res. 32:D104-D108(2004).
CC -----
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CC -----
DR      EMBL; AF550355; AAQ12671.1; -; Genomic_DNA.
FT      NON TER 1
SQ      SEQUENCE 14 AA; 1528 MW; D995F9B3698210B9 CRC64;

Query Match      24.7%; Score 24; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      6 ATNIFYPT 13
        |||
        1 ANNIVPS 8

RESULT 15
O69142_STRPY PRELIMINARY; PRT; 15 AA.
ID O69142_STRPY
AC O69142;
DT 01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT 01-AUG-1998, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE Protein SIC (fragment).
DE Name=sic;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP NUCLEOTIDE SEQUENCE.

```

```

RC      STRAIN=AP1;
RX      MEDLINE=98298075; PubMed=9632622;
RA      Berge A., Rasmussen M., Bjork L.;
RT      "Identification of an insertion sequence located in a region encoding
RT      virulence factors of Streptococcus pyogenes."
RT      Infect. Immun. 66:3449-3453(1998).
RT      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs license
CC      -----
DR      EMBL; AF064540; AAC38769.1; -; Genomic_DNA.
FT      NON TER 1
SQ      SEQUENCE 15 AA; 1552 MW; 87655F847401FF CRC64;

Query Match      24.7%; Score 24; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.2e+04;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy      8 NIPYTPAGT 17
        ::|||
        6 SVTPYTPSAT 15

```

Search completed: May 30, 2006, 15:07:40  
 Job time : 70.6667 secs

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OM protein - protein search, using sw model

Run on: May 30, 2006, 14:59:31 ; Search time 61.6667 Seconds  
(without alignments)  
133.458 Million cell updates/sec

Title: us-10-758-165a-9

Perfect score: 97

Sequence: 1 VDGQKATNIPFYTAQTK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 902922

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_8.\*  
1: Geneseqp1980s.\*  
2: Geneseqp1990s.\*  
3: Geneseqp2000s.\*  
4: Geneseqp2001s.\*  
5: Geneseqp2002s.\*  
6: Geneseqp2003as.\*  
7: Geneseqp2003bs.\*  
8: Geneseqp2004s.\*  
9: Geneseqp2005s.\*  
10: Geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97	100.0	18	ADRI0609	Adri0609 Dog Ige e
2	87	89.7	18	ADRI0610	Adri0610 Cat Ige e
3	55	56.7	18	ADRI0612	Adri0612 Sheep Ige
4	37	38.1	15	ADCS6890	Adcs6890 Peptide f
5	34	35.1	15	ADCS6890	Adcs6890 Horse Imm
6	34	35.1	18	ADRI0611	Adri0611 Horse Ige
7	32.5	33.5	15	ADW78189	Adw78189 Human met
8	32	33.0	9	AAU76520	Aau76520 Anti-Inte
9	32	33.0	9	AAE15818	Aae15818 Human mab
10	32	33.0	9	AAE76312	Aae76312 Prostate
11	32	33.0	11	ADT40399	Adt40399 HSARS vir
12	32	33.0	11	ADT40399	Adt40399 HSARS vir
13	32	33.0	11	ADT40399	Adt40399 HSARS vir
14	32	33.0	11	ADT40399	Adt40399 HSARS vir
15	32	33.0	12	AAAS2787	Aaas2787 CCR5-bind
16	32	33.0	12	AAV13048	Aav13048 Human pho
17	32	33.0	15	AAV65747	Aav65747 Breast ca
18	32	33.0	15	ADN64911	Adn64911 HLA bindi
19	31	32.0	14	ADN64911	Adn64911 HLA bindi
20	31	32.0	15	AAV13329	Aav13329 B. Subtil
21	31	32.0	18	ADN64927	Adn64927 HLA bindi
22	30	30.9	18	ADN64934	Adn64934 Beta-site
23	30	30.9	9	ABJ19961	Abj19961 MHC bindi
			7	ADD94564	Add94564 Human SIM

24	30	30.9	10	7	ADD94544	Add94544 Human SIM
25	30	30.9	14	3	ABJ39162	Abj39162 Human sec
26	30	30.9	14	3	ABJ39162	Abj39162 Human sec
27	30	30.9	16	2	AAJ53562	Aaj53562 Birch pol
28	30	30.9	16	8	ADQ90450	Adq90450 RANTES re
29	30	30.9	17	2	AAJ95159	Aaj95159 bcl-x(l)/
30	29	29.9	9	2	AAW24775	Aaw24775 Human Imm
31	29	29.9	9	2	AAW80144	Aaw80144 Light cha
32	29	29.9	9	2	AAW80142	Aaw80142 Light cha
33	29	29.9	9	2	AAV40427	Aav40427 Amino aci
34	29	29.9	9	5	ABP62411	Abp62411 Human Imm
35	29	29.9	9	6	ABJ26739	Abj26739 VEGF bind
36	29	29.9	9	6	ABR06299	AbR06299 Human can
37	29	29.9	9	8	ADK18234	Adk18234 Mouse VEG
38	29	29.9	9	8	ADV26692	Adv26692 Human 109
39	29	29.9	9	8	ADV29257	Adv29257 Human 109
40	29	29.9	9	9	AEC65856	Aec65856 Human 109
41	29	29.9	9	9	AEC68321	Aec68321 Human 109
42	29	29.9	9	10	AEQ00224	Aeq00224 Kallikrei
43	29	29.9	9	10	AEQ01130	Aeq01130 Kallikrei
44	29	29.9	10	6	ABR06391	AbR06391 Human can
45	29	29.9	10	6	ABR06436	AbR06436 Human can

## ALIGNMENTS

RESULT 1  
ID ADRI0609 standard; peptide; 18 AA.  
XX  
AC ADRI0609;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Dog Ige epitope recognised by monoclonal antibody 3.76, SEQ ID 9.  
XX  
KM Antiasthmatic; Antiallergic; Immunosuppressive; Ige; dog; asthma;  
XX anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.  
XX  
OS Canis familiaris.  
XX  
PN WO2004065936-A2.  
XX  
PD 05-AUG-2004.  
XX  
PF 15-JAN-2004; 2004WO-US003566.  
XX  
PR 16-JAN-2003; 2003US-0440472P.  
XX  
PA (UNIC-) UNIV NORTH CAROLINA STATE.  
XX  
PI Hammerberg B;  
XX  
DR WPI; 2004-593545/57.  
XX  
PT Novel antibody that specifically binds to mammalian Ige epitope, useful  
XX for testing an allergen reactivity of Ige sample, detecting mammalian Ige  
XX or treating asthma or anaphylactic shock.  
XX  
PS Example 6; Page 9; 14pp; English.  
XX  
XX The present invention relates to a novel monoclonal antibody (I) that  
XX specifically binds to a mammalian Ige epitope, where the epitope is  
XX between amino acids 145-166 or 356-374 of mammalian Ige, e.g. dog Ige.  
XX (I) is useful for testing an allergen reactivity of an Ige sample. The  
XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
XX and corn allergens. The sample is a biological sample collected from a  
XX dog, cat or horse. (I) is also useful for detecting mammalian Ige and for  
XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
XX antibodies recognise epitopes on canine Ige corresponding to amino acid  
XX residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
XX canine Ige epsilon-chain. Recognition of epsilon-chains from Ige from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE.

XX Sequence 18 AA;

Query Match 100.0%; Score 97; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 6.5e-09;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAPG 18  
 |||||  
 1 VDGQKATNIFPYTAPG 18

RESULT 2

ADRI0610  
 ID ADRI0610 standard; peptide; 18 AA.

XX ADRI0610;

DT 21-OCT-2004 (first entry)

DE Cat IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 10.

XX Antiasthmatic; Anti-allergic; Immunosuppressive; IGE; dog; asthma;

KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;

KM cat.

XX Felis catus.

OS

XX WO2004065936-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hammerberg B;

XX WPI; 2004-593545/57.

XX Novel antibody that specifically binds to mammalian IGE epitope, useful

PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE

PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

CC The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IGE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
 CC creating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC cat IGE 3.76 recognition site.

XX Sequence 18 AA;

Query Match 89.7%; Score 87; DB 8; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAPG 16  
 |||||  
 1 VDGQKATNIFPYTAPG 16

RESULT 3

ADRI0612  
 ID ADRI0612 standard; peptide; 18 AA.

XX ADRI0612;

DT 21-OCT-2004 (first entry)

DE Sheep IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 12.

XX Antiasthmatic; Anti-allergic; Immunosuppressive; IGE; dog; asthma;

KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;

KM sheep.

XX Ovis aries.

OS

XX WO2004065936-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.

XX (UYNC-) UNIV NORTH CAROLINA STATE.

XX Hammerberg B;

XX WPI; 2004-593545/57.

XX Novel antibody that specifically binds to mammalian IGE epitope, useful

PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE

PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

CC The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IGE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC sheep IGE 3.76 recognition site.

XX Sequence 18 AA;

Query Match 56.7%; Score 55; DB 8; Length 18;  
 Best Local Similarity 66.7%; Pred. No. 0.071;  
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAP 15  
 |||||  
 1 VDGQEDRNLFSYTAP 15

RESULT 4  
 ADIC56890

```

ID ADC56890 standard; peptide; 15 AA.
XX
XX ADC56890;
AC
XX 18-DEC-2003 (first entry)
XX
XX Peptide fragment Seq ID7 related to human protein 36-41.
DE
XX human; protein 36-41; arrhythmia; asthma; dementia.
XX
XX Homo sapiens.
OS
XX CN1382718-A.
XX
XX 04-DEC-2002.
PD
XX 26-APR-2001; 2001CN-00112751.
XX
XX 26-APR-2001; 2001CN-00112751.
XX
XX (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
XX Mao Y, Xie Y;
PI
XX WPI; 2003-269480/27.
XX
XX New human macroprotein-36.41, encoding polynucleotide, antagonist and
PT recombinant production, useful for treating dementia, arrhythmia, asthma
PT and digestive ulcers.
XX
XX Example 6; SEQ ID NO 7; 33pp; Chinese.
XX
XX This invention relates to a novel protein, human protein 36-41, and the
CC DNA sequence encoding it. The protein of the invention may be useful for
CC the treatment of diseases such as arrhythmia, asthma and dementia. The
CC present sequence is the amino acid sequence of a peptide fragment of
CC human protein 36-41 which was used in the exemplification of the
CC invention.
XX
XX Sequence 15 AA;
SQ
Query Match 38.1%; Score 37; DB 7; Length 15;
Best Local Similarity 40.0%; Pred. No. 60;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 VDGQKATNIFPYTAP 15
Db 1 MDGKMQPNSFPWQSP 15

```

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XX
XX Gershwin LJ, Pettigrew HD, Kalina WV;
PI WPI; 2003-765437/72.
XX
XX Immunogenic composition comprising an isolated equine immunoglobulin E
PT polypeptide that induces production of antibodies which specifically bind
PT to equine immunoglobulin E.
XX
XX Example 1; Page 8; 14pp; English.
XX
XX The invention relates to an immunogenic composition comprising an
CC isolated polypeptide having an amino acid sequence that is at least 80%
CC identical to 6 (S1-S6), 15 amino acid peptide sequences derived from
CC equine immunoglobulin E (the composition induces production of an
CC antibody that specifically binds to equine immunoglobulin (Ig)E), the six
CC polypeptides are not explicitly identified in the specification. Also
CC included are a composition comprising an antibody that specifically binds
CC to a polypeptide at least 80% identical to (S1)-(S6), an antibody that
CC specifically binds to equine IgE made by the process of immunising an
CC animal with a polypeptide at least 80% identical to (S1)-(S6), making an
CC antibody that specifically binds to equine IgE (involving immunising an
CC animal with a composition further comprising an isolated polypeptide (the
CC amino acid sequence of the polypeptide is at least 80% identical to (S1)-
CC (S6)), and collecting antiserum from the animal) and a kit for detection
CC of equine IgE in a biological sample comprising the antibody and means
CC for detecting specific binding of the antibody to equine IgE. The
CC antibody is useful for detecting equine IgE protein in a biological
CC sample (serum) which involves contacting the sample with the antibody,
CC thus forming an antigen/antibody complex, and detecting the presence or
CC absence of the antigen/antibody complex. The antibody and antigen are
CC immobilised on a solid surface. The antibody is labelled such that the
CC complex can be detected. The complex is detected using a second labelled
CC antibody. The peptides are useful for generating antibodies specific for
CC IgE which can serve as a diagnostic test for allergy. The present
CC sequence is a Horse immunoglobulin E, IgE, heavy chain immunogenic
CC peptide from the middle portion of the C2 region.
XX
XX Sequence 15 AA;
SQ
Query Match 35.1%; Score 34; DB 7; Length 15;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 VDGQKATNIFP 11
Db 2 IDGKRVDEQFP 12

```

PA (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX  
 XX Hammerberg B;  
 XX  
 DR WPI: 2004-593545/57.  
 XX  
 XX Novel antibody that specifically binds to mammalian Igs epitope, useful  
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
 PT or treating asthma or anaphylactic shock.  
 XX  
 XX Example 6; Page 9; 14pp; English.  
 XX  
 XX The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IGE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC horse IGE 3.76 recognition site.  
 XX  
 XX Sequence 18 AA;  
 XX  
 XX  
 XX Query Match 35.1%; Score 34; DB 8; Length 18;  
 XX Best Local Similarity 54.5%; Pred. No. 2,3e+02;  
 XX Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 XX  
 XX 1 VDGKATNIFP 11  
 XX :||| ||  
 XX 1 IDGKVDQFP 11  
 XX  
 XX  
 XX RESULT 7  
 XX ADW78189  
 XX ID ADW78189 standard; peptide; 15 AA.  
 XX  
 XX AC ADW78189;  
 XX  
 XX DT 07-APR-2005 (first entry)  
 XX  
 XX DE Human metabolic therapy target peptide PACT.  
 XX  
 XX DEF domain; MAP kinase; cytosolic; cardiovascular-gen.; cardiac;  
 KW vasoactive; hypotensive; antiarteriosclerotic; antiinflammatory;  
 KW antiallergic; immunosuppressive; antibacterial; antitumor;  
 KW dermatological; antidiabetic; gastrointestinal-gen.; antileuk;  
 KW chromolytic; neuroprotective; ophthalmological; antihemetic;  
 KW antipyretic; uropathic; antipneumatic; hepatotropic; antianemic;  
 KW muscular-gen.; thyromimetic; antichyroid; gynecological; nephrotropic;  
 KW hepatotropic; virucide; anti-HIV; anabolic; hypertensive; anorectic;  
 KW endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anticonvulsant;  
 KW antidepressant; antidiabetic; sedative; hypnotic; CNS-gen.;  
 KW antileukemia; cancer; cardiovascular disease; inflammation;  
 KW metabolic disorder; neuropathy; sleep disorder.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO2005007090-A2.  
 PN  
 XX  
 XX 27-JAN-2005.  
 PD  
 XX  
 XX 02-JUL-2004; 2004WO-US021514.  
 XX  
 XX 03-JUL-2003; 2003US-0484761P.  
 XX  
 XX

PA (HARD ) HARVARD COLLEGE.  
 XX  
 XX Blenis J, Murphy LO;  
 XX  
 DR WPI: 2005-112720/12.  
 XX  
 XX Identification of compound for treating e.g. cancer by culturing cells  
 PT expressing target protein in the presence of growth factor, cytokine,  
 PT tumor promoter or oncogene and assessing binding after contacting with  
 PT the compound.  
 XX  
 XX Claim 14; Page 64; 104pp; English.  
 XX  
 XX The invention relates to a novel method for the identification of a  
 CC therapeutic compound. The method involves providing test cells that  
 CC express a target protein containing a DEF domain and MAP kinase;  
 CC culturing the cells in the presence of growth factor, cytokine, tumor  
 CC promoter or oncogene; contacting the cells with a candidate compound; and  
 CC assessing the binding of the MAP kinase to the DEF domain relative to the  
 CC binding in the absence of the candidate compound. The invention further  
 CC comprises a method for the identification of a therapeutic compound; a  
 CC method for treatment of cancer, which involves administering a compound  
 CC that inhibits the binding of a MAP kinase to the DEF domain of a target  
 CC protein; and an antibody that specifically binds to phospho-T-325 C-Fos  
 CC (preferably polyclonal or monoclonal). The novel therapeutic compounds  
 CC have the following activities: cytosolic; cardiovascular-gen.; cardiac;  
 CC vasoactive; hypotensive; antiarteriosclerotic; antiinflammatory;  
 CC antiallergic; immunosuppressive; antibacterial; antitumor;  
 CC dermatological; antidiabetic; gastrointestinal-gen.; antileuk;  
 CC chromolytic; neuroprotective; ophthalmological; antihemetic;  
 CC antipyretic; uropathic; antipneumatic; hepatotropic; muscular  
 CC -gen.; thyromimetic; antichyroid; gynecological; nephrotropic;  
 CC hepatotropic; virucide; anti-HIV; anabolic; hypertensive; anorectic;  
 CC endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anticonvulsant;  
 CC antidepressant; antidiabetic; sedative; hypnotic; CNS-gen.; and  
 CC antileukemia. The therapeutic compound may be used in the treatment  
 CC of: cancer, cardiovascular disorders, inflammatory disorders, metabolic  
 CC disorders, neuropathy or a behavioural disorder, and a sleep disorder.  
 CC This sequence represents a metabolic therapy target peptide of the  
 CC invention.  
 XX  
 XX Sequence 15 AA;  
 XX  
 XX  
 XX Query Match 33.5%; Score 32.5; DB 9; Length 15;  
 XX Best Local Similarity 66.7%; Pred. No. 3.4e+02;  
 XX Matches 8; Conservative 0; Mismatches 1; Indels 3; Gaps 1;  
 XX  
 XX 5 KATNIFPYTAPG 16  
 XX :||| ||| ||  
 XX 1 KAT--PYTFPG 9  
 XX  
 XX  
 XX RESULT 8  
 XX AAU76520  
 XX ID AAU76520 standard; peptide; 9 AA.  
 XX  
 XX AC AAU76520;  
 XX  
 XX DT 05-JUN-2002 (first entry)  
 XX  
 XX DE Anti-Interleukin-12 (IL-12) antibody CDR3 light chain.  
 XX  
 XX Human; antibody; anti-interleukin-12; CDR; light chain; circulatory;  
 KW complementarily determining region; neuroprotective; antipneumatic;  
 KW immunostimulant; cytosolic; anti-microbial; psoriasis; infection;  
 KW multiple sclerosis; immune disorder; cardiovascular; malignant disease;  
 KW neurological disorder.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO200212500-A2.  
 PN  
 XX  
 XX 14-FEB-2002.  
 XX  
 XX



XX 07-AUG-2001; 2001WO-US024720.  
 PF 07-AUG-2000; 2000US-0223358P.  
 XX 29-SEP-2000; 2000US-0236827P.  
 PR 01-AUG-2001; 2001US-00920262.  
 XX (CENZ ) CENTOCOR INC.  
 PA  
 XX Giles-Komar J, Knight DM, Peritt D, Scallion B, Shealy D;  
 P1 WPI; 2002-257482/30.  
 XX  
 DR  
 XX New mammalian anti-IL-12 antibodies, useful for diagnosing or treating IL  
 PT -12 related conditions, e.g. psoriasis or multiple sclerosis, as well as  
 PT other for treating immune, infectious, malignant or neurological  
 PT disorders.  
 XX  
 XX Claim 41; Page 93; 96pp; English.  
 PS  
 CC The invention relates to novel isolated mammalian anti-interleukin-12 (IL  
 CC -12) antibodies. The antibodies comprise at least one complementarily  
 CC determining region (CDR) of a heavy or light chain, a heavy chain or  
 CC light chain variable region, or a heavy chain or light chain constant  
 CC region. The anti-IL-12 antibodies are useful in methods for diagnosing or  
 CC treating IL-12 related conditions, e.g. psoriasis or multiple sclerosis.  
 CC The antibodies are also useful for treating immune, cardiovascular,  
 CC infectious, malignant or neurological disorders or diseases. The present  
 CC sequence represents the amino acid sequence of human anti-interleukin-12  
 CC (IL-12) antibody CDR3 light chain  
 XX  
 SO Sequence 9 AA;

Query Match 33.0%; Score 32; DB 5; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 NIPPT 13  
 ||:||||  
 Db 4 NIPPT 9

RESULT 9  
 AAE15818  
 ID AAE15818 standard; peptide; 9 AA.  
 XX  
 AC AAE15818;  
 XX

DT 26-MAR-2002 (first entry)  
 XX

DE Human mAb 12B1 VK complementarily determining region (CDR) #3.  
 XX

XX Human; sialoadhesin factor-3; SAF-3; therapy; cancer; inflammation;  
 KW autoimmunity; allergy; asthma; infection; central nervous system; CNS;  
 KW rheumatoid arthritis; multiple sclerosis; stem cell mobilisation; AIDS;  
 KW haematopoietic development; anaemia; chemoprotective agent; cytostatic;  
 KW immunoglobulin; complementarity determining region; CDR; protozoacide;  
 KW antiinflammatory; immunosuppressive; anti-HIV; antibacterial; virucide;  
 KW fungicide; neuroprotective; light chain variable region; VK; mAb;  
 KW monoclonal antibody.  
 XX

OS Homo sapiens.  
 XX

PN WO200190193-A1.  
 XX

PD 29-NOV-2001.  
 XX

PF 24-MAY-2001; 2001WO-US016864.  
 XX

PR 24-MAY-2000; 2000US-00577930.  
 XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.  
 (SMIK ) SMITHKLINE BEECHAM PLC.  
 PT

XX Abrahamsen JA, Kikly KK;  
 PI WPI; 2002-083094/11.  
 DR  
 XX Novel monoclonal antibody that binds to human sialoadhesin factor-3 for  
 PT treating or preventing cancer, inflammation, autoimmunity, allergy,  
 PT asthma, rheumatoid arthritis, multiple sclerosis, AIDS and infections.  
 XX  
 PS Claim 13; Page 67; 69pp; English.  
 XX

CC The invention relates to monoclonal antibodies that bind to human  
 CC sialoadhesin factor-3 (SAF-3). SAF-3 antibody is useful for treating or  
 CC preventing cancer, inflammation, autoimmunity, allergy, asthma, central  
 CC nervous system (CNS) inflammation, rheumatoid arthritis, multiple  
 CC sclerosis, AIDS and bacterial, fungal, protozoan and viral infections and  
 CC for modulating an immune response in a mammal, where the immune response  
 CC is downregulated or enhanced. SAF-3 antibody is useful as diagnostic and  
 CC therapeutic reagents, to subcharacterise cell populations during  
 CC haematopoietic development, to treat anaemia, as a diagnostic marker to  
 CC distinguish between different forms of cancer, to purge bone marrow ex  
 CC vivo of cancer cells expressing SAF-3, as a tool to aid in the ex vivo  
 CC expansion (proliferation and/or differentiation) of haematopoietic  
 CC progenitor cells expressing SAF-3, as a stimulus in vivo for stem cell  
 CC mobilisation into the periphery and as an vivo chemoprotective agent.  
 CC Protein comprising immunoglobulin complementarily determining region  
 CC (CDR) of SAF-3 antibody and its nucleic acid is useful to configure  
 CC screening methods for detecting the effect of added compounds on the  
 CC production of mRNA and polypeptide in cells. The present sequence is  
 CC complementarily determining region of human monoclonal antibody (mAb)  
 CC 12B1 light chain variable region (VK), which binds to SAF-3  
 XX  
 SO Sequence 9 AA;

Query Match 33.0%; Score 32; DB 5; Length 9;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+06;  
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 NIPPT 13  
 ||:||||  
 Db 4 NIPPT 9

RESULT 10  
 AEF76312  
 ID AEF76312 standard; protein; 9 AA.  
 XX  
 AC AEF76312;  
 XX

DT 20-APR-2006 (first entry)  
 XX

DE Prostate cancer cell antibody light chain CDR3 SEQ ID NO:65.  
 XX

XX antibody; prostate tumor; cytostatic; andrology; genitourinary disease;  
 KW neoplasm; antibody identification; antibody therapy; light chain.  
 XX

OS Mus musculus.  
 XX

PN WO2006017173-A1.  
 XX

PD 16-FEB-2006.  
 XX

PF 08-JUL-2005; 2005WO-US024260.  
 XX

PR 10-JUL-2004; 2004US-0586811P.  
 XX

PA (ALEX-) ALEXION PHARM INC.  
 XX

PI Bowdish KS, Xin H, Yanciri F, Siva A;  
 XX

DR WPI; 2006-173528/18.  
 XX

PT New antibody that binds to a prostate cancer cell, useful for detecting

```

PT  cancerous cells in vivo, for killing or ablating prostate cancer cells in
PS  vivo, and for delivering a variety of cytotoxic drugs.
XX
XX  Claim 16; SEQ ID NO 65; 48bp; English.
XX
XX  The invention relates to an antibody (I) that binds to a prostate cancer
CC  cell. Also described are the following: identifying (M1) antibodies
CC  specific to cancer cells; generating a phage displayed antibody library
CC  using cells collected from subjects immunized with cancer cells; removing
CC  members of the library that bind to human red blood cells to generate a
CC  sub-library, and recovering from the sub-library members that display
CC  antibodies that bind to the cancer cell; or contacting cancer cells with
CC  a hapten, generating a phage displayed antibody library using cells
CC  collected from subjects immunized with cancer cells, removing members of
CC  the library that bind to human red blood cells to generate a sub-library,
CC  and recovering from the sub-library members that display antibodies that
CC  bind to the cancer cell; an isolated nucleic acid (II) encoding (I); an
CC  expression vector (III) comprising (II); a host cell (IV) transfected
CC  with (III); and an antibody that binds to Cdcpl. (M1) is useful for
CC  identifying antibodies specific to cancer cells. (I) is useful as a
CC  therapeutic for cancer, for detecting cancerous cells in vivo, for
CC  killing or ablating cancerous cells in vivo (preferably prostate cancer
CC  cells), and for delivering a variety of cytotoxic drugs including
CC  therapeutic drugs, a compound emitting radiation, molecules of plants,
CC  fungal or bacterial origin, biological proteins, and their mixtures. The
CC  present sequence represents prostate cancer cell antibody light chain
CC  CD33 SEQ ID NO:65.
XX
XX  Sequence 9 AA;
SQ
XX
XX  Query Match          33.0%; Score 32; DB 10; Length 9;
XX  Best Local Similarity 83.3%; Pred. No. 2.1e+06;
XX  Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
OY      8 NIPPYT 13
XX      ||:||
XX      4 NIPPYT 9
XX
Db
XX
XX  RESULT 11
XX  ADT40399
XX  ID      ADT40399 standard; peptide; 11 AA.
XX  AC
XX  ADT40399;
XX  DT      30-DEC-2004 (first entry)
XX  XX
XX  hSARS virus peptide, SEQ ID 1387.
XX  DE
XX  SARS virus peptide, SEQ ID 1387.
XX  KW
XX  Virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.
XX  OS
XX  SARS coronavirus.
XX  PN      WO2004085650-A1.
XX  PD
XX  07-OCT-2004.
XX  PF
XX  24-MAR-2004; 2004WO-CN000246.
XX  XX
XX  24-MAR-2003; 2003US-0457031P.
XX  PR  26-MAR-2003; 2003US-0457730P.
XX  PR  02-APR-2003; 2003US-0459931P.
XX  PR  03-APR-2003; 2003US-0460357P.
XX  PR  08-APR-2003; 2003US-0461265P.
XX  PR  14-APR-2003; 2003US-0462805P.
XX  PR  23-APR-2003; 2003US-0464866P.
XX  PR  25-APR-2003; 2003US-0465738P.
XX  PR  14-MAY-2003; 2003US-0470935P.
XX  XX
XX  (U7HK-) UNIV HONG KONG.
XX  PI      Chen K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K,
XX  Leung FC;

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XX  DR      WPI; 2004-737326/72.
XX  XX
XX  PT      New nucleic acid molecule encoding nucleocapsid- or spike-gene protein of
XX  PT      a human Severe Acute Respiratory Syndrome (hSARS) virus, useful for
XX  PT      diagnosing and treating SARS.
XX  PS      Example; SEQ ID NO 1387; 200bp; English.
XX  XX
XX  XX  The present invention relates to novel human Severe Acute Respiratory
CC  Syndrome (hSARS) viral nucleic acid and protein sequences derived from a
CC  hSARS virus having China Center for Type Culture Collection Deposit
CC  Accession No. C27CC-V200303. The present invention also relates to novel
CC  nucleic acid molecules (I; ADT41483 or ADT41485) encoding a nucleocapsid-
CC  (N) or spike (S)-gene protein of a hSARS virus. Also disclosed are
CC  methods for detecting the presence of a N- or S-gene of the hSARS virus
CC  or of the protein in a biological sample and identifying a subject
CC  infected with the hSARS virus. The hSARS virus, nucleic acid and protein
CC  sequences are useful as vaccines for diagnosing or treating SARS. They
CC  are also useful in clinical and scientific research applications. The
CC  hSARS virus genome (ADT39027) was obtained and the amino acid sequences
CC  of all three reading frames were deduced from the complementary strand.
CC  ADT40120 is the full-length protein encoded by the first reading frame of
CC  the complementary strand and ADT40121-ADT40601 are the peptides from the
CC  first reading frame protein. ADT40602 is the full-length protein encoded
CC  by the second reading frame of the complementary strand and ADT40603-
CC  ADT40976 are the peptides from the second reading frame protein. ADT40977
CC  is the full-length protein encoded by the third reading frame of the
CC  complementary strand and ADT40978-ADT41482 are the peptides from the
CC  third reading frame protein.
XX
XX  Sequence 11 AA;
SQ
XX
XX  Query Match          33.0%; Score 32; DB 8; Length 11;
XX  Best Local Similarity 54.5%; Pred. No. 3e+02;
XX  Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
OY      3 GOKATNIPPYT 13
XX      ||:||
XX      1 GOSGSIIPPT 11
XX
Db
XX
XX  RESULT 12
XX  ADS79816
XX  ID      ADS79816 standard; protein; 11 AA.
XX  AC
XX  ADS79816;
XX  DT      30-DEC-2004 (first entry)
XX  XX
XX  SARS virus complementary DNA strand reading frame 1 protein #279.
XX  DE
XX  SARS virus complementary DNA strand reading frame 1 protein #279.
XX  KW
XX  virucide; vaccine; detection; severe acute respiratory syndrome;
XX  real-time quantitative polymerase chain reaction; SARS.
XX  OS
XX  SARS coronavirus.
XX  PN      WO2004085455-A1.
XX  PD
XX  07-OCT-2004.
XX  PF
XX  24-MAR-2004; 2004WO-CN000247.
XX  XX
XX  24-MAR-2003; 2003US-0457031P.
XX  PR  26-MAR-2003; 2003US-0457730P.
XX  PR  02-APR-2003; 2003US-0459931P.
XX  PR  03-APR-2003; 2003US-0460357P.
XX  PR  08-APR-2003; 2003US-0461265P.
XX  PR  14-APR-2003; 2003US-0462805P.
XX  PR  23-APR-2003; 2003US-0464866P.
XX  PR  05-MAY-2003; 2003US-0468139P.
XX  PR  16-MAY-2003; 2003US-0471200P.
XX  XX

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PA (UYHK-) UNIV HONG KONG.  
XX  
PI Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;  
XX  
DR WPI; 2004-737292/72.  
XX  
PT New isolated nucleic acid molecule useful for detecting, treating,  
PT ameliorating, or preventing the virus causing severe acute respiratory  
PT syndrome in humans using a real-time quantitative polymerase chain  
PT reaction assay.  
XX  
PS Example; SEQ ID NO 1387; 183bp; English.  
XX  
CC The invention relates to an isolated nucleic acid molecule consisting  
CC essentially of, and/or hybridizes under stringent conditions to a fully  
CC defined nucleotide sequence of 16-25 base pairs (bp); SEQ ID NO: 2471-  
CC 2476), or its complement. The methods and compositions of the present  
CC invention are useful for the detection of the virus causing Severe Acute  
CC Respiratory Syndrome (SARS) in humans using a real-time quantitative  
CC polymerase chain reaction (PCR) assay. They can also be used in treating,  
CC ameliorating, managing or preventing SARS. This sequence corresponds to a  
CC partial SARS protein sequence from the complementary reading frame 1.  
XX  
SQ Sequence 11 AA;  
  
Query Match 33.0%; Score 32; DB 8; Length 11;  
Best Local Similarity 54.5%; Pred. No. 3e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
QY 3 GOKATNIFPYT 13  
Db 1 GOSOSNINPOT 11  
  
RESULT 13  
ADT37929  
ID ADT37929 standard; peptide; 11 AA.  
XX  
AC ADT37929;  
XX  
DT 30-DEC-2004 (first entry)  
XX  
DE hSARS virus peptide, SEQ ID 1387.  
XX  
KM Virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.  
XX  
OS SARS coronavirus.  
XX  
PN WO2004085633-A1.  
XX  
PD 07-OCT-2004.  
XX  
PE 24-MAR-2004; 2004WO-CN000248.  
XX  
PR 24-MAR-2003; 2003US-0457031P.  
PR 26-MAR-2003; 2003US-0457730P.  
PR 02-APR-2003; 2003US-0459931P.  
PR 03-APR-2003; 2003US-0460357P.  
PR 08-APR-2003; 2003US-0461265P.  
PR 14-APR-2003; 2003US-0462805P.  
PR 23-APR-2003; 2003US-0464886P.  
XX  
PA (UYHK-) UNIV HONG KONG.  
XX  
PI Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;  
XX  
DR WPI; 2004-728736/71.  
XX  
PT New isolated human severe acute respiratory syndrome (hSARS) virus,  
PT useful as vaccine for diagnosing or treating SARS or in clinical and  
PT scientific research applications.  
XX

PS Example; SEQ ID NO 1387; 176bp; English.  
XX  
CC The present invention relates to novel human Severe Acute Respiratory  
CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a  
CC hSARS virus having China Center for Type Culture Collection Deposit  
CC Accession No. CCRCC-V200303. The hSARS virus, nucleic acid and protein  
CC sequences are useful as vaccines for diagnosing or treating SARS. They  
CC are also useful in clinical and scientific research applications. The  
CC hSARS virus genome (ADT36557) was obtained and the amino acid sequences  
CC of all three reading frames were deduced from the complementary strand.  
CC ADT37650 is the full-length protein encoded by the first reading frame of  
CC the complementary strand and ADT37651-ADT38131 are the peptides from the  
CC first reading frame protein. ADT38132 is the full-length protein encoded  
CC by the second reading frame of the complementary strand and ADT38133-  
CC ADT38506 are the peptides from the second reading frame protein. ADT38507  
CC is the full-length protein encoded by the third reading frame of the  
CC complementary strand and ADT38508-ADT39012 are the peptides from the  
CC third reading frame protein.  
XX  
SQ Sequence 11 AA;  
  
Query Match 33.0%; Score 32; DB 8; Length 11;  
Best Local Similarity 54.5%; Pred. No. 3e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
  
QY 3 GOKATNIFPYT 13  
Db 1 GOSOSNINPOT 11  
  
RESULT 14  
AAM52787  
ID AAM52787 standard; peptide; 12 AA.  
XX  
AC AAM52787;  
XX  
DT 22-FEB-2002 (first entry)  
XX  
DE CCR5-binding phage display peptide #4.  
XX  
KM CCR5 binding peptide; CC chemokine receptor 5; human; HIV infection;  
KM human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;  
KM drug screening; identification; phage display library.  
XX  
OS Synthetic.  
XX  
PN WO200171346-A2.  
XX  
PD 27-SEP-2001.  
XX  
PE 21-MAR-2001; 2001WO-US009155.  
XX  
PR 21-MAR-2000; 2000US-0190946P.  
PR 21-MAR-2000; 2000US-0190996P.  
PR 21-MAR-2000; 2000US-0191299P.  
PR 20-MAR-2001; 2001US-00813448.  
PR 20-MAR-2001; 2001US-00813651.  
PR 20-MAR-2001; 2001US-00813653.  
XX  
PA (CONS-) CONSENSUS PHARM INC.  
XX  
PI Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;  
XX  
DR WPI; 2002-010610/01.  
XX  
PT Identifying CC chemokine receptor 5 binding compound for treating AIDS,  
PT comprises binding a molecule from library to a molecule having binding  
PT property corresponding to CCR5 and identifying bound molecule.  
XX  
PS Claim 20; Page 33; 50pp; English.  
XX  
CC The invention relates to a method for identifying a binding compound for  
CC CC chemokine receptor 5 (CCR5). The method involves screening a library

CC of test molecules (particularly peptides) with immobilised CCR5, and then  
CC identifying those molecules which bind. The invention also relates to  
CC CCR5-binding molecules identified using the method of the invention,  
CC methods for identifying consensus motifs for CCR5-binding peptides, a  
CC transfer vector encoding tagged CCR5, a computer-aided method for  
CC determining the relative binding affinity of a test molecule to CCR5 and  
CC a computer aided drug screening assay that utilises the three-dimensional  
CC structure of CCR5. Compounds identified using the methods of the  
CC invention are useful for treating or preventing HIV (human  
CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency  
CC syndrome) in a patient. The methods of the invention may also be used to  
CC identify agonists or antagonists of the interaction of CCR5 with its  
CC natural ligand, and to determine a binding motif for CCR5. Sequences  
CC AAM52784-AAM52805 and AAM52814 represent specifically claimed CCR5-  
CC binding peptides identified using methods of the invention  
XX  
SQ Sequence 12 AA;  
Query Match 33.0%; Score 32; DB 5; Length 12;  
Best Local Similarity 62.5%; Pred. No. 3.3e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 10 PPYRPGT 17  
:|:|:|  
4 YPYGAPRT 11  
RESULT 15  
ADV13048  
ID ADV13048 standard; peptide; 12 AA.  
XX  
AC ADV13048;  
XX  
DT 10-MAR-2005 (first entry)  
XX  
DE Human phosphorylated peptide from phosphoprotein #986.  
XX  
KW Alzheimer disease; neuroprotective; nootropic; degeneration; tumor;  
KW neoplasm; neurological disease; phosphorylation; protein sequencing;  
KW phosphoprotein.  
XX  
OS Homo sapiens.  
XX  
PN W02004108948-A2.  
XX  
PD 16-DEC-2004.  
XX  
PF 04-JUN-2004; 2004WO-US017613.  
XX  
PR 04-JUN-2003; 2003US-0476010P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
XX  
PI Gyg1 SP;  
XX  
DR WPI; 2005-031720/03.  
XX  
PT Characterizing phosphorylated polypeptides in a sample comprises  
PT digesting the polypeptides with a protease thus generating test peptides,  
PT and collecting a fraction of test peptides that enriched for positively  
PT charged peptides.  
XX  
PS Claim 16; Page 79; 123pp; English.  
XX  
CC The invention relates to characterizing phosphorylated polypeptides in a  
CC sample comprising digesting the polypeptides with a protease thus  
CC generating test peptides, and collecting a fraction of test peptides that  
CC enriched for positively charged peptides. Also included are a method  
CC (comprising determining the presence, absence or level of one ore more  
CC phosphorylated peptides as identified above in cells having a cell state  
CC and determining the degree of correlation between the presence, absence  
CC or level of phosphorylated polypeptide with the cell state), an isolated  
CC peptide of 5-50 amino acids comprising an amino acid sequence that is a

CC subsequence of any of the protein sequences given in the specification  
CC (and which comprise a phosphorylation site within the subsequence), an  
CC isolated polypeptide selected from any of the polypeptides listed in the  
CC specification and is modified at a modification site, an isolated peptide  
CC comprising a mass spectral peak signatures, a method for identifying a  
CC treatment that modulates phosphorylation of an amino acid in a target  
CC polypeptide, a method for generating a peptide standard, a pair of  
CC peptide standards comprising the peptide obtained (where the peptide is  
CC phosphorylated and a corresponding peptide comprising an identical amino  
CC acid sequence but which is not phosphorylated), a system (comprising a  
CC computer memory comprising data files storing information relating to the  
CC identifying characteristics of positively charged peptides), and a data  
CC analysis module capable of executing instructions for organizing and/or  
CC searching the data files), a computer program product (comprising data  
CC relating to the identifying characteristics of positively charged  
CC peptides and comprising instructions for organizing and/or searching the  
CC data), and a method for characterizing N-terminal peptides in a sample. The  
CC method is useful for characterizing phosphorylated polypeptides in a  
CC sample. The present sequence is a peptide from a human phosphoprotein,  
CC containing a phosphorylation site, identified by the method of the  
CC invention.  
XX  
SQ Sequence 12 AA;  
Query Match 33.0%; Score 32; DB 9; Length 12;  
Best Local Similarity 85.7%; Pred. No. 3.3e+02;  
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 11 PYTAPGT 17  
|:|:|:|  
3 PATAPGT 9

Search completed: May 30, 2006, 15:04:08  
Job time : 64.6667 secs

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OW protein - protein search, using sw model

Run on: May 30, 2006, 15:17:23 ; Search time 49.3333 Seconds  
(without alignments)  
169.011 Million cell updates/sec

Title: US-10-758-165A-9  
Perfect score: 97  
Sequence: 1 VDGOKATNIFPYTAGTK 18

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

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Maximum DB seq length: 18

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*  
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6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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1	97	100.0	18	US-10-758-165-9	Sequence 9, Appl
2	87	89.7	18	US-10-758-165-10	Sequence 10, Appl
3	55	56.7	18	US-10-758-165-12	Sequence 12, Appl
4	37	38.1	15	US-10-856-118-34	Sequence 34, Appl
5	34	35.1	15	US-10-052-788-5	Sequence 5, Appl
6	34	35.1	18	US-10-758-165-11	Sequence 11, Appl
7	32	33.0	9	US-09-920-262A-6	Sequence 6, Appl
8	32	33.0	9	US-10-912-994-6	Sequence 6, Appl
9	32	33.0	9	US-10-975-883-6	Sequence 6, Appl
10	32	33.0	9	US-10-975-740A-6	Sequence 6, Appl
11	32	33.0	9	US-10-975-708-6	Sequence 6, Appl
12	32	33.0	9	US-10-246-019A-14	Sequence 14, Appl
13	32	33.0	11	US-10-808-187-1387	Sequence 1387, Ap
14	32	33.0	11	US-10-807-807-1387	Sequence 1387, Ap
15	32	33.0	11	US-11-004-399-2080	Sequence 2080, Ap
16	32	33.0	12	US-09-813-653-26	Sequence 26, Appl
17	32	33.0	12	US-10-862-195-1037	Sequence 1037, Ap
18	32	33.0	15	US-10-776-224-64	Sequence 64, Appl
19	32	33.0	15	US-10-530-061-1511	Sequence 1511, Ap
20	31	32.0	13	US-10-300-694A-64	Sequence 64, Appl
21	31	32.0	14	US-09-229-751A-16	Sequence 16, Appl
22	31	32.0	15	US-10-530-061-1527	Sequence 1527, Ap
23	31	32.0	18	US-10-685-898-81	Sequence 81, Appl
24	30	30.9	9	US-09-865-548A-126	Sequence 126, App
25	30	30.9	9	US-10-705-459-126	Sequence 126, App
26	30	30.9	18	US-10-195-730-360	Sequence 360, App
27	30	30.9	18	US-10-799-747-360	Sequence 360, App

28	30	30.9	18	US-10-979-183-360	Sequence 360, App
29	29	29.9	9	US-10-482-430-40	Sequence 40, Appl
30	29	29.9	9	US-11-009-840A-214	Sequence 214, App
31	29	29.9	9	US-11-009-873A-214	Sequence 214, App
32	29	29.9	9	US-11-009-769A-214	Sequence 214, App
33	29	29.9	12	US-10-894-672-39	Sequence 39, Appl
34	29	29.9	12	US-10-996-316-39	Sequence 39, Appl
35	29	29.9	12	US-11-171-567-39	Sequence 39, Appl
36	29	29.9	15	US-10-783-455-9	Sequence 9, Appl
37	29	29.9	15	US-10-720-831-20	Sequence 20, Appl
38	29	29.9	17	US-09-992-896-51	Sequence 51, Appl
39	29	29.9	17	US-10-306-631-76	Sequence 76, Appl
40	29	29.9	18	US-10-846-548A-1	Sequence 1, Appl
41	28	28.9	9	US-10-160-506-34	Sequence 34, Appl
42	28	28.9	9	US-10-449-379-34	Sequence 34, Appl
43	28	28.9	9	US-10-688-015-34	Sequence 34, Appl
44	28	28.9	9	US-10-160-505-34	Sequence 34, Appl
45	28	28.9	9	US-10-482-284A-186	Sequence 186, App

## ALIGNMENTS

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RESULT 1
US-10-758-165-9
; Sequence 9, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-9

Query Match      100.0%  Score 97;  DB 5;  Length 18;
Best Local Similarity 100.0%  Pred. No. 1e-08;
Matches 18;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      1 VDGOKATNIFPYTAGTK 18
Db      1 VDGOKATNIFPYTAGTK 18

RESULT 2
US-10-758-165-10
; Sequence 10, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-10

Query Match      89.7%  Score 87;  DB 5;  Length 18;

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Best Local Similarity 100.0%; Pred. No. 4.4e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIPYTPAG 16  
|||||

DB 1 VDGOKATNIPYTPAG 16  
|||||

## RESULT 3

US-10-758-165-12  
; Sequence 12, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hamnerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 12  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-10-758-165-12

Query Match 56.7%; Score 55; DB 5; Length 18;  
Best Local Similarity 66.7%; Pred. No. 0.079;  
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDGOKATNIPYTPAP 15  
|||||

DB 1 VDGOKATNIPYTPAP 15  
|||||

## RESULT 4

US-10-856-118-34  
; Sequence 34, Application US/10856118  
; Publication No. US20050025747A1  
; GENERAL INFORMATION:  
; APPLICANT: Laidlaw, Stephen  
; APPLICANT: Skinner, Mike  
; APPLICANT: Hill, Adrian V.S.  
; APPLICANT: Anderson, Richard  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: 3742.1000-000  
; CURRENT APPLICATION NUMBER: US/10/856,118  
; CURRENT FILING DATE: 2004-05-27  
; PRIOR APPLICATION NUMBER: PCT/GB02/005411  
; PRIOR FILING DATE: 2002-12-02  
; PRIOR APPLICATION NUMBER: GB0128733.3  
; PRIOR FILING DATE: 2001-11-30  
; PRIOR APPLICATION NUMBER: US 60/334,649  
; PRIOR FILING DATE: 2001-11-30  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Flanking sequence  
US-10-856-118-34

Query Match 38.1%; Score 37; DB 5; Length 15;  
Best Local Similarity 55.6%; Pred. No. 58;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 TNNIPYTPAP 15  
|||

DB 2 TNNIPYDVP 10  
|||||

## RESULT 5

US-10-052-788-5  
; Sequence 5, Application US/10052788  
; Publication No. US20030087314A1  
; GENERAL INFORMATION:  
; APPLICANT: Gershwin, Laurel J.  
; APPLICANT: Pettigrew, Howard David  
; APPLICANT: Kallina, Warren V.  
; TITLE OF INVENTION: The Regents of the University of California  
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for  
; FILE REFERENCE: 023070-121000US  
; CURRENT APPLICATION NUMBER: US/10/052,788  
; CURRENT FILING DATE: 2001-11-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: epitope peptide  
; OTHER INFORMATION: p5, middle portion of C2 of equine IGE epsilon  
US-10-052-788-5

Query Match 35.1%; Score 34; DB 4; Length 15;  
Best Local Similarity 54.5%; Pred. No. 1.8e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDGOKATNIPF 11  
|||||

DB 2 IDGQKVDQFP 12  
|||||

## RESULT 6

US-10-758-165-11  
; Sequence 11, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hamnerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 11  
; LENGTH: 18  
; TYPE: PRT  
; ORGANISM: Equus caballus  
US-10-758-165-11

Query Match 35.1%; Score 34; DB 5; Length 18;  
Best Local Similarity 54.5%; Pred. No. 2.2e+02;  
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDGOKATNIPF 11  
|||||

DB 1 IDGQKVDQFP 11  
|||||

## RESULT 7

US-09-920-262A-6  
; Sequence 6, Application US/09920262A  
; Publication No. US20030124123A1  
; GENERAL INFORMATION:  
; APPLICANT: Shealy, David

Wed May 31 06:05:28 2006

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; APPLICANT: Knight, David
; APPLICANT: Scallon, Bernie
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Pettit, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920,262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-09-920-262A-6

```

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Query Match          33.0%; Score 32; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

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QY      8 NIPYPT 13
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        4 NIPYPT 9
DB

```

```

RESULT 8
US-10-912-994-6
; Sequence 6, Application US/10912994
; Publication No. US2005002937A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Knight, David
; APPLICANT: Pettit, David
; APPLICANT: Scallon, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248DIY1
; CURRENT APPLICATION NUMBER: US/10/912,994
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-912-994-6

```

```

Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```
QY      8 NIPYPT 13
        ||:||||
        4 NIPYPT 9
DB

```

```

RESULT 9
US-10-975-883-6
; Sequence 6, Application US/10975883
; Publication No. US2005011217A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Knight, David

```

```

; APPLICANT: Pettit, David
; APPLICANT: Scallon, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND USES
; FILE REFERENCE: CEN0248DIY04
; CURRENT APPLICATION NUMBER: US/10/975,883
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-975-883-6

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```

Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```
QY      8 NIPYPT 13
        ||:||||
        4 NIPYPT 9
DB

```

```

RESULT 10
US-10-975-740A-6
; Sequence 6, Application US/10975740A
; Publication No. US2005019683A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Knight, David
; APPLICANT: Pettit, David
; APPLICANT: Scallon, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND NUCLEIC ACIDS
; FILE REFERENCE: CEN0248DIY03
; CURRENT APPLICATION NUMBER: US/10/975,740A
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
;
US-10-975-740A-6

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Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```
QY      8 NIPYPT 13
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        4 NIPYPT 9
DB

```

```

RESULT 11
US-10-975-708-6
; Sequence 6, Application US/10975708
; Publication No. US20050214293A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill

```

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; APPLICANT: Knight, David
; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND COMPOSITIONS
; FILE REFERENCE: CEN0248DI02
; CURRENT APPLICATION NUMBER: US/10/975,708
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-708-6

Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred.No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      8 NIPYPT 13
        ||:||||
        4 NIPYPT 9

Db

RESULT 12
US-10-246-019A-14
; Sequence 14, Application US/10246019A
; Publication No. US20060073133A1
; GENERAL INFORMATION:
; APPLICANT: Kikly, Kristine K.
; APPLICANT: Abrahamson, Julie
; TITLE OF INVENTION: Sialoschesin Factor-3 Antibodies
; FILE REFERENCE: GH50019-1C1
; CURRENT APPLICATION NUMBER: US/10/246,019A
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: USSN 09/577,930
; PRIOR FILING DATE: 2000-01-22
; PRIOR APPLICATION NUMBER: USSN 09/046,736
; PRIOR FILING DATE: 1998-03-24
; PRIOR APPLICATION NUMBER: USSN 60/041,885
; PRIOR FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human
US-10-246-019A-14

Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred.No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      8 NIPYPT 13
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        4 NIPYPT 9

Db

RESULT 13
US-10-808-187-1387
; Sequence 1387, Application US/10808187
; Publication No. US2005000909A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
```

```

; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1387
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-1387

Query Match          33.0%; Score 32; DB 5; Length 11;
Best Local Similarity 54.5%; Pred.No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      3 GOKANTNIPYPT 13
        ||:||||
        1 GOSOSNIPPT 11

Db

RESULT 14
US-10-807-807-1387
; Sequence 1387, Application US/10807807
; Publication No. US20050181357A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; FILE REFERENCE: V9661.0077
; CURRENT APPLICATION NUMBER: US/10/807,807
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 60/464,886
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; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/465,738
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/470,935
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1387
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-807-807-1387

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Query Match          33.0%; Score 32; DB 5; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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```

QY      3 GQKATNIPPYT 13
      ||:|||||
Db      1 GQSOSNIPQT 11

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RESULT 15
US-11-004-399-2080
; Sequence 2080, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Wee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-COV Viral Nucleotide
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399
; PRIOR FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2080
; LENGTH: 11
; TYPE: PRT
; ORGANISM: SARS-COV VIRUS
US-11-004-399-2080

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Query Match          33.0%; Score 32; DB 6; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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```

QY      3 GQKATNIPPYT 13
      ||:|||||
Db      1 GQSOSNIPQT 11

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OM protein - protein search, using sw model

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(without alignments)  
50.118 Million cell updates/sec

Title: US-10-758-165A-9  
Perfect score: 97  
Sequence: 1 VDGQKATNIPFYTAPGTX 18

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 1113735 residues

Total number of hits satisfying chosen parameters: 11661

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
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- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEM\_PUB pep.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEM\_PUB pep.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/PCR\_NEM\_PUB pep.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEM\_PUB pep.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEM\_PUB pep.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEM\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28.9	9	7	US-11-219-563-34	Sequence 34, Appl
2	26.8	9	7	US-11-254-182-12	Sequence 12, Appl
3	24.7	16	1	US-09-731-899-19	Sequence 19, Appl
4	23.7	9	6	US-10-522-356-3	Sequence 3, Appl
5	23.7	9	7	US-11-252-276-38	Sequence 38, Appl
6	23.7	9	7	US-11-023-959A-83	Sequence 83, Appl
7	23.7	10	6	US-10-538-066-747	Sequence 747, Appl
8	23.7	10	7	US-11-219-563-16	Sequence 16, Appl
9	23.7	12	7	US-11-106-014-82	Sequence 82, Appl
10	23.7	12	7	US-11-177-358C-16	Sequence 16, Appl
11	23.7	12	7	US-11-177-359C-16	Sequence 16, Appl
12	23.7	12	7	US-11-177-340C-16	Sequence 16, Appl
13	23.7	12	7	US-11-122-986-799	Sequence 799, Appl
14	23.7	13	7	US-11-134-228A-8	Sequence 8, Appl
15	23.7	17	7	US-11-257-498-59	Sequence 59, Appl
16	23.7	17	7	US-11-121-282-63	Sequence 63, Appl
17	23.7	17	7	US-11-251-734-30	Sequence 30, Appl
18	23.7	18	7	US-11-257-498-53	Sequence 53, Appl
19	22.7	9	7	US-11-297-317-21	Sequence 21, Appl
20	22.7	9	7	US-11-140-487A-211	Sequence 211, Appl
21	22.7	9	7	US-11-140-487A-348	Sequence 348, Appl
22	22.7	10	7	US-11-140-487A-1314	Sequence 1314, Appl
23	22.7	10	7	US-11-140-487A-1346	Sequence 1346, Appl
24	22.7	11	6	US-10-540-431-5	Sequence 5, Appl
25	22.7	12	7	US-11-122-986-656	Sequence 656, Appl

26	22.7	17	7	US-11-121-482-52	Sequence 52, Appl
27	21.6	9	7	US-11-055-093-222	Sequence 222, Appl
28	21.6	9	7	US-11-140-487A-120	Sequence 120, Appl
29	21.6	9	7	US-11-140-487A-551	Sequence 551, Appl
30	21.6	9	7	US-11-140-487A-1214	Sequence 1214, Appl
31	21.6	10	7	US-11-055-093-223	Sequence 223, Appl
32	21.6	10	7	US-11-140-487A-1596	Sequence 1596, Appl
33	21.6	11	6	US-10-540-431-11	Sequence 11, Appl
34	21.6	11	7	US-11-177-358C-3	Sequence 3, Appl
35	21.6	11	7	US-11-177-358C-3	Sequence 3, Appl
36	21.6	11	7	US-11-177-358C-3	Sequence 3, Appl
37	21.6	12	1	US-09-784-950-21	Sequence 21, Appl
38	20.6	9	6	US-10-538-066-7	Sequence 7, Appl
39	20.6	9	6	US-10-538-066-8	Sequence 8, Appl
40	20.6	9	7	US-11-140-487A-8	Sequence 8, Appl
41	20.6	9	7	US-11-140-487A-24	Sequence 24, Appl
42	20.6	9	7	US-11-140-487A-212	Sequence 212, Appl
43	20.6	9	7	US-11-140-487A-327	Sequence 327, Appl
44	20.6	9	7	US-11-140-487A-443	Sequence 443, Appl
45	20.6	9	7	US-11-140-487A-472	Sequence 472, Appl

## ALIGNMENTS

RESULT 1  
US-11-219-563-34  
; Sequence 34, Application US/11219563  
; Publication No. US20060088539A1  
; GENERAL INFORMATION:  
; APPLICANT: Bandet, Neil  
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF  
; FILE REFERENCE: 13651.001 (BZL-001)  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US/11/219,563  
; PRIOR FILING DATE: 2004-03-03  
; PRIOR APPLICATION NUMBER: US 10/379,838  
; PRIOR FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: 10/449,379  
; PRIOR FILING DATE: 2003-05-30  
; NUMBER OF SEQ ID NOS: 144  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-11-219-563-34  
  
Query Match 28.9%; Score 28; DB 7; Length 9;  
Best Local Similarity 63.6%; Pred. No. 5.2e+04;  
Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 1;  
  
QY 3 GOKATNIPFYT 13  
DB 1 GOSYT--FPYT 9  
  
RESULT 2  
US-11-254-182-12  
; Sequence 12, Application US/11254182  
; Publication No. US20060088523A1  
; GENERAL INFORMATION:  
; APPLICANT: ANDYA, JAMES  
; APPLICANT: GMEB, SHIANG C.  
; APPLICANT: LIU, JUN  
; APPLICANT: SHEN, YE  
; TITLE OF INVENTION: ANTIBODY FORMULATIONS  
; FILE REFERENCE: P2104R1  
; CURRENT APPLICATION NUMBER: US/11/254,182  
; CURRENT FILING DATE: 2005-10-19  
; PRIOR APPLICATION NUMBER: US 60/620,413

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; PRIOR FILING DATE: 2004-10-20
; NUMBER OF SEQ ID NOS: 74
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-254-182-12

Query Match                26.8%; Score 26; DB 7; Length 9;
Best Local Similarity      80.0%; Pred. No. 5.2e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      9 IFPYT 13
       1:|1|1|
       5 IYPYT 9

Db

RESULT 3
US-09-731-899-19
; Sequence 19, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
; APPLICANT: Chai, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREOF, AND METHODS
; FILE REFERENCE: 20555/1203433-US1
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,687
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Tetanus toxin bacteria
US-09-731-899-19

Query Match                24.7%; Score 24; DB 1; Length 16;
Best Local Similarity      44.4%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      7 TNIFPYTAP 15
       1:|1|1|1|
       3 STVPIYIGP 11

Db

RESULT 4
US-10-522-356-3
; Sequence 3, Application US/10522356
; Publication No. US20060105323A1
; GENERAL INFORMATION:
; APPLICANT: WHITEHEAD, CHRISTOPHER BRUCE ALEXANDER
; APPLICANT: CLARK, ANTHONY JOHN
; APPLICANT: MOLE, CHARLES ROLAND
; TITLE OF INVENTION: MULTI-REPORTER GENE MODEL FOR TOXICOLOGICAL SCREENING
; FILE REFERENCE: 102286.155 US1
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: PCT/GB03/003192
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: GB 0217402.7
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Sequence: Haemagglutinin
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; OTHER INFORMATION: epitope from unknown organism
US-10-522-356-3

Query Match                23.7%; Score 23; DB 6; Length 9;
Best Local Similarity      50.0%; Pred. No. 5.2e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      10 FPYTAP 15
       1:|1|1|1|
       1 YPYDVP 6

Db

RESULT 5
US-11-252-276-38
; Sequence 38, Application US/11252276
; Publication No. US20060094868A1
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Bright, Gary
; APPLICANT: Olson, Keith
; APPLICANT: Burroughs-Tencza, Sarah
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-K2-CO
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: 09/713,572
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: 09/430,656
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/398,965
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 09/031,271
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: 08/810,983
; PRIOR FILING DATE: 1997-02-27
; PRIOR APPLICATION NUMBER: 60/136,078
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 60/106,308
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA epitope
US-11-252-276-38

Query Match                23.7%; Score 23; DB 7; Length 9;
Best Local Similarity      50.0%; Pred. No. 5.2e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      10 FPYTAP 15
       1:|1|1|1|
       1 YPYDVP 6

Db

RESULT 6
US-11-023-959A-83
; Sequence 83, Application US/11023959A
; Publication No. US20060106203A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; TITLE OF INVENTION: Ligand
; FILE REFERENCE: 8039/2142
; CURRENT FILING DATE: 2004-12-28
; PRIOR APPLICATION NUMBER: PCT/GB03/002804
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 83
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LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: HA tag  
US-11-023-959A-83

Query Match 23.7%; Score 23; DB 7; Length 9;  
Best Local Similarity 50.0%; Pred. No. 5.2e+04;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 PPYAP 15  
: |||  
Db 1 YPYDVP 6

RESULT 7  
US-10-538-066-747  
Sequence 747, Application US/10538066  
Publication No. US20060094649A1  
GENERAL INFORMATION:  
APPLICANT: Eptimmune Inc.  
TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen  
TITLE OF INVENTION: Peptides and Compositions  
FILE REFERENCE: 2060.015PC06  
CURRENT APPLICATION NUMBER: US/10/538,066  
CURRENT FILING DATE: 2005-06-09  
PRIOR APPLICATION NUMBER: US 60/432,017  
PRIOR FILING DATE: 2002-12-10  
NUMBER OF SEQ ID NOS: 767  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 747  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Unknown  
FEATURE:  
OTHER INFORMATION: A3 non-natural consensus peptide  
US-10-538-066-747

Query Match 23.7%; Score 23; DB 6; Length 10;  
Best Local Similarity 75.0%; Pred. No. 1.9e+02;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 IFPY 12  
: |||  
Db 2 VFPPY 5

RESULT 8  
US-11-219-563-16  
Sequence 16, Application US/11219563  
Publication No. US20060088539A1  
GENERAL INFORMATION:  
APPLICANT: Bander, Neil  
TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC  
TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF  
FILE REFERENCE: 13651.001 (BZL-001)  
CURRENT APPLICATION NUMBER: US/11/219,563  
CURRENT FILING DATE: 2005-09-02  
PRIOR APPLICATION NUMBER: PCT/US04/06586  
PRIOR FILING DATE: 2004-03-03  
PRIOR APPLICATION NUMBER: US 10/379,838  
PRIOR FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: 10/449,379  
PRIOR FILING DATE: 2003-05-30  
NUMBER OF SEQ ID NOS: 144  
SOFTWARE: PaateSeq for Windows Version 4.0  
SEQ ID NO 16  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: deimmunized light chain J591

US-11-219-563-16

Query Match 23.7%; Score 23; DB 7; Length 10;  
Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PGTK 18  
: |||  
Db 3 PGTK 6

RESULT 9  
US-11-106-014-82  
Sequence 82, Application US/11106014  
Publication No. US2006008846A1  
GENERAL INFORMATION:  
APPLICANT: Pagano, Michele  
APPLICANT: Chiau, Dah Shaim  
APPLICANT: Latres, Esther  
APPLICANT: Srivastava, Promod  
APPLICANT: Chandawarkar, Rajiv  
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT  
TITLE OF INVENTION: OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS  
FILE REFERENCE: 5914-106-999  
CURRENT APPLICATION NUMBER: US/11/106,014  
CURRENT FILING DATE: 2005-04-13  
PRIOR APPLICATION NUMBER: 10/632,150  
PRIOR FILING DATE: 2003-07-30  
PRIOR APPLICATION NUMBER: 10/042,417  
PRIOR FILING DATE: 2002-01-07  
PRIOR APPLICATION NUMBER: 09/385,219  
PRIOR FILING DATE: 1999-08-27  
PRIOR APPLICATION NUMBER: 60/118,568  
PRIOR FILING DATE: 1999-02-03  
PRIOR APPLICATION NUMBER: 60/098,355  
PRIOR FILING DATE: 1998-08-28  
PRIOR APPLICATION NUMBER: 60/124,449  
PRIOR FILING DATE: 1997-03-15  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 82  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-106-014-82

Query Match 23.7%; Score 23; DB 7; Length 12;  
Best Local Similarity 46.2%; Pred. No. 2.3e+02;  
Matches 6; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 2 DQKATNIPYTA 14  
: ||| : |||  
Db 2 DGEKDT--YSYLA 12

RESULT 10  
US-11-177-358C-16  
Sequence 16, Application US/11177358C  
Publication No. US20060094072A1  
GENERAL INFORMATION:  
APPLICANT: CAMPBELL, DOUGLAS A.  
TITLE OF INVENTION: PEPTIDE SEQUENCE TAGS AND METHOD OF USING SAME  
FILE REFERENCE: 113703-1006  
CURRENT APPLICATION NUMBER: US/11/177,358C  
CURRENT FILING DATE: 2005-07-11  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 16  
LENGTH: 12  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

US-11-177-358C-16

Query Match 23.7%; Score 23; DB 7; Length 12;  
Best Local Similarity 57.1%; Pred. No. 2.3e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 PPYTAPG 16  
DB 1 FPCDGP 7

RESULT 11

US-11-177-359C-16  
; Sequence 16, Application US/11177359C  
; Publication No. US20060094058A1  
; GENERAL INFORMATION:  
; APPLICANT: CAMPBELL, DOUGLAS A.  
; TITLE OF INVENTION: PEPTIDE SEQUENCE TAGS AND METHOD OF USING SAME  
; FILE REFERENCE: 113703-1004  
; CURRENT APPLICATION NUMBER: US/11/177,359C  
; CURRENT FILING DATE: 2005-07-11  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
US-11-177-359C-16

Query Match 23.7%; Score 23; DB 7; Length 12;  
Best Local Similarity 57.1%; Pred. No. 2.3e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 PPYTAPG 16  
DB 1 FPCDGP 7

RESULT 12  
US-11-177-340C-16  
; Sequence 16, Application US/11177340C  
; Publication No. US20060099663A1  
; GENERAL INFORMATION:  
; APPLICANT: CAMPBELL, DOUGLAS A.  
; TITLE OF INVENTION: PEPTIDE SEQUENCE TAGS AND METHOD OF USING SAME  
; FILE REFERENCE: 113703-1005  
; CURRENT APPLICATION NUMBER: US/11/177,340C  
; CURRENT FILING DATE: 2005-07-11  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide  
US-11-177-340C-16

Query Match 23.7%; Score 23; DB 7; Length 12;  
Best Local Similarity 57.1%; Pred. No. 2.3e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 PPYTAPG 16  
DB 1 FPCDGP 7

RESULT 13  
US-11-122-986-799  
; Sequence 799, Application US/11122986  
; Publication No. US20060104989A1

; GENERAL INFORMATION:  
; APPLICANT: EDWARDS, ALED  
; APPLICANT: DHARAMSI, AKIL  
; APPLICANT: VEDADI, MASOUD  
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES  
; FILE REFERENCE: IPT-330.01  
; CURRENT APPLICATION NUMBER: US/11/122,986  
; CURRENT FILING DATE: 2005-05-05  
; PRIOR APPLICATION NUMBER: 60/423,875  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 60/423,832  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 60/423,915  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 60/423,757  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 60/423,758  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: 60/424,367  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/424,376  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/424,370  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/424,362  
; PRIOR FILING DATE: 2002-11-06  
; PRIOR APPLICATION NUMBER: 60/424,373  
; PRIOR FILING DATE: 2002-11-06  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 844  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 799  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Streptococcus pneumoniae  
US-11-122-986-799

Query Match 23.7%; Score 23; DB 7; Length 12;  
Best Local Similarity 61.5%; Pred. No. 8.3e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 2;

QY 7 TNIPYT-APGTX 18  
DB 1 SNI-PYTWGGRK 12

RESULT 14  
US-11-134-228A-8  
; Sequence 8, Application US/11134228A  
; Publication No. US20060105320A1  
; GENERAL INFORMATION:  
; APPLICANT: Lindquist et al.  
; TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS  
; FILE REFERENCE: 30554/40155A  
; CURRENT APPLICATION NUMBER: US/11/134,228A  
; CURRENT FILING DATE: 2005-05-20  
; PRIOR APPLICATION NUMBER: 60/573,277  
; PRIOR FILING DATE: 2004-05-20  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Hemagglutinin  
US-11-134-228A-8

Query Match 23.7%; Score 23; DB 7; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.5e+02;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Wed May 31 06:05:28 2006

QY 10 FPYTAP 15  
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Db 1 YPYDVP 6

RESULT 15  
US-11-257-498-59

; Sequence 59, Application US/11257498  
; Publication No. US20060088550A1  
; GENERAL INFORMATION:  
; APPLICANT: Bachmann, Martin F  
; APPLICANT: Pulurija, Alma  
; APPLICANT: Saudan, Philippe  
; TITLE OF INVENTION: Gastric Inhibitory Polypeptide (GIP) Antigen Arrays and Used therefor  
; FILE REFERENCE: 1700.0540001  
; CURRENT APPLICATION NUMBER: US/11/257,498  
; PRIOR FILING DATE: 2005-10-25  
; PRIOR APPLICATION NUMBER: 60/621,465  
; PRIOR FILING DATE: 2004-10-25  
; NUMBER OF SEQ ID NOS: 76  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 59  
; LENGTH: 17  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: CGGPKPSTPPGSSGGAP  
US-11-257-498-59

## Query Match

23.7%; Score 23; DB 7; Length 17;

Best Local Similarity 57.1%; Pred. No. 3.3e+02; Indels 0; Gaps 0;

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Db 6 PSTPPGS 12

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Job time : 4 secs

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Wed May 31 06:05:24 2006

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OM protein - protein search, using sw model

Run on: May 30, 2006, 09:59:16 ; Search time 20.3333 Seconds  
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Title: US-10-758-165A-3

Perfect score: 74

Sequence: 1 RNNVLIQDQQTTR 15

Scoring table: BLOSUM62

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Listing first 45 summaries

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2: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/6.COMB.pep:\*  
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7: /EMC\_Celerra\_SIDS3/ptodata/2/iaa/backfltest.pep:\*Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	37.8	10	3	US-09-641-528B-4809
2	28	37.8	11	3	US-09-641-528B-4810
3	28	37.8	11	3	US-09-641-528B-4856
4	28	37.8	11	3	US-09-641-528B-13626
5	28	37.8	11	3	US-09-641-528B-26703
6	28	37.8	15	3	US-09-641-528B-47147
7	28	37.8	15	3	US-09-641-528B-50653
8	26	35.1	9	3	US-09-641-528B-4922
9	26	35.1	9	3	US-09-641-528B-50984
10	26	35.1	10	3	US-09-641-528B-9923
11	26	35.1	10	3	US-09-641-528B-26799
12	25	33.8	14	2	US-09-236-415-6
13	25	33.8	15	1	US-08-221-583-42
14	25	33.8	15	5	PCT-US95-04018-42
15	25	33.8	11	1	US-08-456-6708-38
16	24	32.4	11	2	US-09-372-036-38
17	24	32.4	13	2	US-10-112-582A-14
18	24	32.4	15	1	US-08-403-378B-7
19	24	32.4	15	3	US-09-641-528B-46828
20	23	31.1	8	3	US-09-641-528B-4862
21	23	31.1	9	3	US-09-641-528B-4808
22	23	31.1	9	3	US-09-641-528B-4863
23	23	31.1	9	3	US-09-641-528B-13652
24	23	31.1	9	3	US-09-641-528B-26750
25	23	31.1	10	2	US-08-485-324-4
26	23	31.1	10	2	US-08-485-324-30

27	23	31.1	10	2	US-08-447-906-4	Sequence 4, Appl
28	23	31.1	10	2	US-08-447-506-10	Sequence 30, Appl
29	23	31.1	10	2	US-08-235-437-4	Sequence 4, Appl
30	23	31.1	10	2	US-08-235-437-30	Sequence 30, Appl
31	23	31.1	10	2	US-08-447-515-4	Sequence 4, Appl
32	23	31.1	10	2	US-08-447-515-30	Sequence 4, Appl
33	23	31.1	10	2	US-09-462-645C-29	Sequence 29, Appl
34	23	31.1	10	2	US-09-573-830-30	Sequence 4, Appl
35	23	31.1	10	2	US-09-573-830-30	Sequence 30, Appl
36	23	31.1	10	3	US-09-641-528B-4855	Sequence 4855, Ap
37	23	31.1	11	3	US-09-641-528B-4860	Sequence 4860, Ap
38	23	31.1	12	1	US-08-479-233-8	Sequence 8, Appl
39	23	31.1	12	2	US-09-392-812A-7	Sequence 7, Appl
40	23	31.1	12	5	PCT-US93-00643-8	Sequence 8, Appl
41	23	31.1	14	2	US-10-394-980-55	Sequence 55, Appl
42	23	31.1	15	2	US-09-700-993-6	Sequence 6, Appl
43	22	29.7	5	1	US-08-762-106-19	Sequence 19, Appl
44	22	29.7	5	2	US-09-320-774-19	Sequence 19, Appl
45	22	29.7	6	1	US-08-762-106-17	Sequence 17, Appl

## ALIGNMENTS

```
RESULT 1
US-09-641-528B-4809
; Sequence 4809, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Estebean
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4809
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-4809
;
Query Match          37.8%; Score 28; DB 3; Length 10;
Best Local Similarity 40.0%; Pred. No. 70;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY      5 LIQDQQT 14
Db      1 MVQVEQQTT 10
RESULT 2
US-09-641-528B-4810
; Sequence 4810, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Estebean
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
```

```

; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4810
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-4810

Query Match      37.8%; Score 28; DB 3; Length 11;
Best Local Similarity 40.0%; Pred. No. 78;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      5 LIOTDQACTT 14
Db      1 MVOVEEQOTT 10

RESULT 3
US-09-641-528B-4856
; Sequence 4856, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4856
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-4856

Query Match      37.8%; Score 28; DB 3; Length 11;
Best Local Similarity 40.0%; Pred. No. 78;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      5 LIOTDQACTT 14
Db      2 MVOVEEQOTT 11

RESULT 4
US-09-641-528B-13626
; Sequence 13626, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard

; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13626
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-13626

Query Match      37.8%; Score 28; DB 3; Length 11;
Best Local Similarity 40.0%; Pred. No. 78;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      5 LIOTDQACTT 14
Db      1 MVOVEEQOTT 10

RESULT 5
US-09-641-528B-26703
; Sequence 26703, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 26703
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-26703

Query Match      37.8%; Score 28; DB 3; Length 11;
Best Local Similarity 40.0%; Pred. No. 78;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      5 LIOTDQACTT 14
Db      1 MVOVEEQOTT 10

RESULT 6
US-09-641-528B-47147
; Sequence 47147, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
```

```

; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 47147
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-47147

Query Match          37.8%; Score 28; DB 3; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 LIOTDOQATT 14
   :|:|:|
Db 1 MVEVEQOTT 10

RESULT 7
US-09-641-528B-50653
; Sequence 50653, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 50653
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-50653

Query Match          37.8%; Score 28; DB 3; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 LIOTDOQATT 14
   :|:|:|
Db 3 MVEVEQOTT 12

RESULT 8
US-09-641-528B-4922
; Sequence 4922, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert

; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4922
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-4922

Query Match          35.1%; Score 26; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 5e+05;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 IOTDOQATT 14
   :|:|:|
Db 1 VVEVEQOTT 9

RESULT 9
US-09-641-528B-50984
; Sequence 50984, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 50984
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-50984

Query Match          35.1%; Score 26; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 5e+05;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 IOTDOQATT 14
   :|:|:|
Db 1 VVEVEQOTT 9

RESULT 10
US-09-641-528B-4923
; Sequence 4923, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
```

```

: APPLICANT: Chesnut, Robert
: APPLICANT: Cells, Esteban
: TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
: FILE REFERENCE: 2060.0100001
: CURRENT FILING DATE: 1999-01-25
: PRIOR APPLICATION NUMBER: US/09/641,528B
: PRIOR FILING DATE: 1999-12-10
: NUMBER OF SEQ ID NOS: 51505
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 4923
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-4923
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```

Query Match      35.1%; Score 26; DB 3; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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```
Qy      6 IOTDOQATT 14
      :|::|||
Db      1 VQVEQQT 9
```

```

RESULT 11
US-09-641-528B-26799
: Sequence 26799, Application US/09641528B
: Patent No. 7026443
: GENERAL INFORMATION:
: APPLICANT: Sette, Alessandro
: APPLICANT: Sidney, John
: APPLICANT: Southwood, Scott
: APPLICANT: Chesnut, Robert
: APPLICANT: Cells, Esteban
: APPLICANT: Grey, Howard
: TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
: FILE REFERENCE: 2060.0100001
: CURRENT APPLICATION NUMBER: US/09/641,528B
: CURRENT FILING DATE: 2000-08-15
: PRIOR APPLICATION NUMBER: US 60/172,705
: PRIOR FILING DATE: 1999-12-10
: NUMBER OF SEQ ID NOS: 51505
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 26799
: LENGTH: 10
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-26799
```

```

Query Match      35.1%; Score 26; DB 3; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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```
Qy      6 IOTDOQATT 14
      :|::|||
Db      1 VQVEQQT 9
```

```

RESULT 12
US-09-236-415-6
: Sequence 6, Application US/09236415
: Patent No. 6309863
: GENERAL INFORMATION:
: APPLICANT: Anderson, Carl W.
: APPLICANT: Appella, Ettore
```

```

: APPLICANT: Sakaguchi, Kazuasu
: TITLE OF INVENTION: METHODS FOR GENERATING PHOSPHORYLATION SITE-SPECIFIC
: FILE REFERENCE: U.S. Application 09/236,415
: CURRENT APPLICATION NUMBER: US/09/236,415
: CURRENT FILING DATE: 1999-01-25
: NUMBER OF SEQ ID NOS: 10
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 6
: LENGTH: 14
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: POLYPEPTIDE
: OTHER INFORMATION: ANTIGEN
: FEATURE:
: OTHER INFORMATION: Residue Xaa is a phosphoserine mimetic
US-09-236-415-6
```

```

Query Match      33.8%; Score 25; DB 2; Length 14;
Best Local Similarity 54.5%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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```
Qy      2 NNVLIOQTDOQA 12
      :|::|||
Db      3 NNVLXPLPSQA 13
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```

RESULT 13
US-08-221-583-42
: Sequence 42, Application US/08221583
: Patent No. 5486595
: GENERAL INFORMATION:
: APPLICANT: Heavenr, George A.
: TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
: NUMBER OF SEQUENCES: 62
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595-r18
: STREET: One Liberty Place 46th Floor
: CITY: Philadelphia
: STATE: Pennsylvania
: COUNTRY: USA
: ZIP: 19403
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25.mdcmod.
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/221,583
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Deluca, Mark
: REGISTRATION NUMBER: 33,229
: REFERENCE/DOCKET NUMBER: CCOR-0185
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-3100
: TELEFAX: (215) 568-3439
: INFORMATION FOR SEQ ID NO: 42:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 15 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-221-583-42
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```

Query Match      33.8%; Score 25; DB 1; Length 15;
Best Local Similarity 55.6%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

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Qy      7 QTDQQATTR 15
      :|::|||
```

Db 4 QVETOATR 12

RESULT 14  
PCT-US95-04018-42  
Sequence 42, Application PC/TUS9504018  
GENERAL INFORMATION:  
APPLICANT: Heavner, George A.  
APPLICANT: Kruszyński, Marian  
APPLICANT: Mervic, Miljenko  
APPLICANT: Weber, Robert W.  
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors  
NUMBER OF SEQUENCES: 76  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
STREET: One Liberty Place 46th Floor  
CITY: Philadelphia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19403  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04018  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/221,580  
FILING DATE: 01-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/221,583  
FILING DATE: 01-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/221,581  
FILING DATE: 01-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: CCOR-0232  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US95-04018-42

Query Match 33.8%; Score 25; DB 5; Length 15;  
Best Local Similarity 55.6%; Pred. No. 3.9e+02;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 QDOOATTR 15  
| : |||  
Db 4 QVETOATR 12

RESULT 15  
US-08-456-670B-38  
Sequence 38, Application US/08456670B  
Patent No. 5932415  
GENERAL INFORMATION:  
APPLICANT: SCHUBERT, PETER  
APPLICANT: NEUMANN, SIEGFRIED  
APPLICANT: PAMELZIK, MARTINA  
APPLICANT: LINKEWILLER, WINFRIED  
APPLICANT: BURGER, CHRISTA

APPLICANT: HOFMANN, GOTTFRIED  
APPLICANT: RUBERT, ANDREAS  
APPLICANT: GOEBEL, WERNER  
APPLICANT: KOHLER, STEFAN  
TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING  
TITLE OF INVENTION: LISTERIAS  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.  
STREET: 2200 CLARENDON BLVD., SUITE 1400  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: US  
ZIP: 22201  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/456,670B  
FILING DATE: 01-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/412,227  
FILING DATE: 27-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/075,248  
FILING DATE: 11-JUN-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 4239567.4  
FILING DATE: 25-NOV-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 421911.4  
FILING DATE: 11-JUN-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: HAMLET-KING, DIANA  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: MERCK 1694D1  
TELEPHONE: 703-243-6333  
TELEFAX: 703-243-6410  
TELEX: 64191  
INFORMATION FOR SEQ ID NO: 38:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
ORIGINAL SOURCE:  
ORGANISM: Listeria innocua  
US-08-456-670B-38

Query Match 32.4%; Score 24; DB 1; Length 11;  
Best Local Similarity 57.1%; Pred. No. 4.2e+02;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 9 DOOATTR 15  
| : |||  
Db 1 EQOTTK 7

Search completed: May 30, 2006, 11:11:06  
Job time : 20.3333 secs

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GenCore version 5.1.8  
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# OM protein - protein search, using sw model

Run on: May 30, 2006, 09:58:55 ; Search time 11.6667 Seconds  
(without alignments)  
123.707 Million cell updates/sec

Title: US-10-758-165A-3  
Sequence: 1 RNNVLITQDDQATTR 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80:\*

1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	33.8	15	2	S32677
2	21	28.4	13	2	B61458
3	21	28.4	13	2	B61458
4	21	28.4	15	2	PH1329
5	20	27.0	10	2	S43625
6	19	25.7	10	2	A53695
7	19	25.7	13	2	H56046
8	19	25.7	14	2	C44823
9	18	24.3	9	2	S6636
10	18	24.3	11	2	S43626
11	18	24.3	13	2	A58491
12	18	24.3	15	2	PT0205
13	18	24.3	15	2	S72432
14	17	23.0	10	2	A61354
15	17	23.0	10	2	PH0933
16	17	23.0	11	2	G42762
17	17	23.0	11	4	S52252
18	17	23.0	12	4	A40763
19	17	23.0	13	2	S36887
20	17	23.0	13	2	E42762
21	17	23.0	13	2	PCI008
22	17	23.0	13	2	I49637
23	17	23.0	14	2	PH1705
24	17	23.0	14	2	PH0753
25	17	23.0	14	2	D35141
26	17	23.0	15	2	PA0058
27	17	23.0	15	2	D56385
28	17	23.0	15	2	S62641
29	17	23.0	15	2	B46047

30	16	21.6	10	2	D54823	olfactory receptor
31	16	21.6	10	2	C54823	olfactory receptor
32	16	21.6	11	2	S70720	trigger factor hom
33	16	21.6	12	2	A53099	163K exoantigen -
34	16	21.6	13	2	S28425	20K protein - rape
35	16	21.6	14	2	E81280	probable proteolys
36	16	21.6	15	2	P00681	photosystem I 19.0
37	16	21.6	15	2	P80452	32K protein 306 -
38	16	21.6	15	2	PH1631	Ig H chain V-D-J r
39	16	21.6	15	2	A45096	thyrotropin-releas
40	16	21.6	15	2	A36527	juvenile-hormone e
41	16	21.6	15	2	A53594	calnexin - mouse (
42	16	20.3	8	2	S71919	alcohol dehydrogen
43	15	20.3	8	2	T48890	hypothetical prote
44	15	20.3	10	2	P00788	NADH2 dehydrogenas
45	15	20.3	11	2	P00682	photosystem I 17.5

## ALIGNMENTS

RESULT 1  
S32677  
nitrogenase cofactor synthesis protein nifs - Anabaena variabilis (fragment)  
N:Contains: L-cysteine sulfuryltransferase (EC 2.8.1.-)  
C:Species: Anabaena variabilis  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C:Accession: S32677  
R:Monerjahn, U.; Boehme, H.  
Submitted to the EMBL Data Library, December 1992  
A:Description: Cloning and expression in E. coli of the Anabaena.  
A:Reference number: S32675  
A:Accession: S32677  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-15 <MON>  
A:Cross-references: UNIPROT:Q44507; UNIPARC:UPI00001301C; EMBL:X69898; NID:G296503; PID  
C:Superfamily: nitrogen fixation protein nifs  
C:Keywords: sulfurtransferase

Query Match 33.8%; Score 25; DB 2; Length 15;  
Best Local Similarity 45.5%; Pred. No. 2.1e+02;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 LIOTDQATTR 15  
DB 3 VIYLDNNATTK 13

RESULT 2  
B61458  
Ig kappa chain V-I region (BLA) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 16-Aug-1996  
R:Bronev, J.C.; Delaghi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Minaesco, E.  
U. Exp. Med. 170, 1551-1558, 1989  
A:Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-asso  
A:Reference number: A61458; MUID:90039128; PMID:2478651  
A:Accession: B61458  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-13 <BRO>  
A:Cross-references: UNIPARC:UPI000017C25D  
C:Keywords: heterotrimer; immunoglobulin

Query Match 28.4%; Score 21; DB 2; Length 13;  
Best Local Similarity 55.6%; Pred. No. 1e+03;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 IOTDQATTT 14  
DB 2 IQMTSPPTT 10

RESULT 3  
A61458  
Ig kappa chain V-I region (BCU) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 15-Oct-1994 #sequence\_revision 15-Oct-1994 #text\_change 16-Aug-1996  
C/Accession: A61458; PL0156  
R/Brouet, J.C.; Delagrè, K.; Gendron, M.C.; Chevaller, A.; Schmitt, C.; Mihaesco, E.  
J. Exp. Med. 170, 1551-1558, 1994  
A/Title: Expression of a public Idiotypic by human monoclonal IGM directed to myelin-assc  
A/Reference number: A61458; MUID:90039128; PMID:2478651  
A/Accession: A61458  
A/Molecule type: protein  
A/Residues: 1-13 <BRO>  
A/Cross-references: UNIPARC:UPI000017C25E  
C/Comment: This protein is one of monoclonal IGM reactive with myeloma-associated glycop  
C/Keywords: heterotetramer; immunoglobulin

Query Match 28.4%; Score 21; DB 2; Length 13;  
Best Local Similarity 55.6%; Pred. No. 1e+03;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 6 IQTDOQATT 14  
|||  
Db 2 IQMTOSPTT 10

RESULT 4  
PH1329  
Ig heavy chain DJ region (clone C552-104) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH1329  
R/Masberman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A/Reference number: PH1302; MUID:93094761; PMID:1460419  
A/Accession: PH1329  
A/Molecule type: DNA  
A/Residues: 1-15 <WAS>  
A/Cross-references: UNIPARC:UPI000017C245  
C/Keywords: heterotetramer; immunoglobulin

Query Match 28.4%; Score 21; DB 2; Length 15;  
Best Local Similarity 66.7%; Pred. No. 1.2e+03;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNNVLI 6  
|||  
Db 4 RNEVMI 9

RESULT 5  
S43625  
cytochrome-c oxidase (EC 1.9.3.1) chain Va, hepatic - rainbow trout (fragment)  
C/Species: Oncorhynchus mykiss (rainbow trout)  
C/Date: 20-Oct-1994 #sequence\_revision 01-Nov-1996 #text\_change 09-Jul-2004  
C/Accession: S43625  
R/Freund, R.; Kadenbach, B.  
Eur. J. Biochem. 221, 1111-1116, 1994  
A/Title: Identification of tissue-specific isoforms for subunits Vb and V1a of cytochr  
A/Reference number: S43624; MUID:94237150; PMID:8181469  
A/Accession: S43625  
A/Molecule type: protein  
A/Residues: 1-10 <FRE>  
A/Cross-references: UNIPROT:P80328; UNIPARC:UPI0000128131  
A/Note: the source is designated as Salmo gairdneri  
C/Genetics:  
A/Genome: nuclear  
C/Keywords: liver; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 27.0%; Score 20; DB 2; Length 10;

Best Local Similarity 33.3%; Pred. No. 1.2e+03;  
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 6 IQTDOQ 11  
:::  
Db 5 VETDER 10

RESULT 6  
A55695  
proteoglycan core protein - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 01-Dec-1995 #sequence\_revision 01-Dec-1995 #text\_change 17-Mar-1999  
C/Accession: A55695  
R/Lark, M.W.; Gordy, J.T.; Weidner, J.R.; Ayala, J.; Kimura, J.H.; Williams, H.R.; Mumfo  
J. Biol. Chem. 270, 2550-2556, 1995  
A/Title: Cell-mediated catabolism of aggrecan. Evidence that cleavage at the "aggrecana  
A/Reference number: A55695; MUID:95155314; PMID:7852317  
A/Accession: A55695  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <LAR>  
A/Cross-references: UNIPARC:UPI000017C9A9

Query Match 25.7%; Score 19; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 1.8e+03;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNNVLI 6  
|||  
Db 2 RGNVIL 7

RESULT 7  
H56046  
urinary tract stone matrix protein 10, 42K - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 09-Jul-2004  
C/Accession: H56046  
R/Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.  
submitted to the Protein Sequence Database, February 1995  
A/Description: Isolation, characterization and sequence of stone proteins.  
A/Reference number: A56046  
A/Accession: H56046  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-13 <BIN>  
A/Cross-references: UNIPROT:Q7M4P7; UNIPARC:UPI000017C406

Query Match 25.7%; Score 19; DB 2; Length 13;  
Best Local Similarity 37.5%; Pred. No. 2.5e+03;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 2 NNVLIQTD 9  
:::  
Db 6 NDLAERFD 13

RESULT 8  
C44823  
synaptoosomal-associated protein SNAP-25 peptide 8 - rabbit (fragment)  
N/Alternate names: superprotein peptide 8  
C/Species: Oryctolagus cuniculus (domestic rabbit)  
C/Date: 31-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 15-Jun-1996  
C/Accession: C44823  
R/Lewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.  
J. Neurosci. 11, 3412-3421, 1991  
A/Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is  
A/Reference number: A44823; MUID:92044785; PMID:1941090  
A/Accession: C44823  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-14 <LOE>



A:Cross-references: UNIPARC:UPI000017C5E7

A:Experimental source: visual tissue

A>Note: sequence extracted from NCBI backbone (NCBIP:64253)

C:Keywords: membrane trafficking

Query Match 25.7%; Score 19; DB 2; Length 14;

Best Local Similarity 42.9%; Pred. No. 2.7e+03; Indels 0; Gaps 0;

Matches 3; Conservative 2; Mismatches 2; Indels 0;

Oy 5 LVLTDDQ 11

Db 2 LVMLDEQ 8

RESULT 9

S66636 alpha-2-macroglobulin isoform 2 - bovine (fragment)

C:Species: Bos primigenius indicus (zebu cattle)

C>Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004

C:Accession: S66636

R:DOImer: K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottrup

FEBS Lett. 372, 93-95, 1995

A>Title: Crystallization and preliminary X-ray analysis of the receptor-binding domain c

A:Reference number: S66634; MUID:96032553; PMID:7556651

A:Accession: S66636

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-9 <DOL>

A:Cross-references: UNIPROT:Q7M2N7; UNIPARC:UPI000017C480

Query Match 24.3%; Score 18; DB 2; Length 9;

Best Local Similarity 37.5%; Pred. No. 2.8e+05; Indels 0; Gaps 0;

Matches 3; Conservative 3; Mismatches 2; Indels 0;

Oy 3 NVLIQTDQ 10

Db 2 NILPKDE 9

RESULT 10

S43626 cytochrome-c oxidase (EC 1.9.3.1) chain Vb-H - trout (fragment)

C:Species: Salmo sp. (trout)

C>Date: 19-Mar-1997 #sequence\_revision 01-Aug-1997 #text\_change 02-Jul-1998

C:Accession: S43626

R:Freund, R.; Kadenbach, B.

Eur. J. Biochem. 221, 1111-1116, 1994

A>Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome

A:Reference number: S43624; MUID:94237150; PMID:8181469

A:Accession: S43626

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-11 <PRE>

A:Cross-references: UNIPARC:UPI000017BF62

C:Keywords: electron transfer; membrane-associated complex; oxidoreductase; respiratory

Query Match 24.3%; Score 18; DB 2; Length 11;

Best Local Similarity 50.0%; Pred. No. 3.2e+03; Indels 0; Gaps 0;

Matches 3; Conservative 2; Mismatches 1; Indels 0;

Oy 6 IOTDDQ 11

Db 6 IPTDEE 11

RESULT 11

A59491 epithelial dog allergen - Canis familiaris (fragment)

C:Species: Canis familiaris

C>Date: 27-Oct-2003 #sequence\_revision 27-Oct-2003 #text\_change 27-Oct-2003

C:Accession: A59491

R:Saarelainen, S.; Taitainen, A.; Rytkk-vnen-Misinen, M.; Auriola, S.; Immonen, A.; MM-

submitted to the Protein Sequence Database, October 2003

A:Description: Diagnosis of dog allergy with recombinant allergens.

A:Reference number: A59491

A:Accession: A59491

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <VIR>

A>Note: IGE-binding protein; allergen

Query Match 24.3%; Score 18; DB 2; Length 13;

Best Local Similarity 80.0%; Pred. No. 3.8e+03; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 1; Indels 0;

Oy 3 NVLIQ 7

Db 3 NVLTQ 7

RESULT 12

PT0205 insulin-like growth factor-binding protein, bone - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 08-Dec-1994

C:Accession: PT0205; A33175

R:Bautista, C.M.; Baylink, D.J.; Mohan, S.

Biochem. Biophys. Res. Commun. 176, 756-763, 1991

A>Title: Isolation of a novel insulin-like growth factor (IGF) binding protein from huma

A:Reference number: PT0205; MUID:9122244; PMID:1709017

A:Accession: PT0205

A:Molecule type: protein

A:Residues: 1-15 <BAU>

A:Cross-references: UNIPARC:UPI000017C275

Query Match 24.3%; Score 18; DB 2; Length 15;

Best Local Similarity 33.3%; Pred. No. 4.5e+03; Indels 0; Gaps 0;

Matches 3; Conservative 3; Mismatches 3; Indels 0;

Oy 4 VLIOTDDQ 12

Db 5 VAVEPDDKA 13

RESULT 13

S72432 epoxyp propane isomerase component B - Xanthobacter sp. (strain Py2) (fragment)

C:Species: Xanthobacter sp.

A:Variety: strain Py2

C>Date: 14-Apr-1998 #sequence\_revision 08-May-1998 #text\_change 07-May-1999

C:Accession: S72432

R:Chan Kwo Chion, C.K.N.; Leak, D.J.

Biochem. J. 319, 489-506, 1996

A>Title: Purification and characterization of two components of epoxyp propane isomerase/c

A:Reference number: S72431; MUID:97069704; PMID:8912687

A:Accession: S72432

A:Molecule type: protein

A:Residues: 1-15 <CHA>

A:Cross-references: UNIPARC:UPI000017CA9F

A>Note: 3-Met and 13-Leu were also found

C:Complex: homodimer

C:Function:

A:Description: NADP-dependent lipamide reductase

A:Pathway: epoxyp propane degradation

A>Note: sensitive to N-ethyl-maleimide and p-chloromercuribenzoate

C:Keywords: FAD

Query Match 24.3%; Score 18; DB 2; Length 15;

Best Local Similarity 44.4%; Pred. No. 4.5e+03; Indels 0; Gaps 0;

Matches 4; Conservative 2; Mismatches 3; Indels 0;

Oy 1 RNNVLIQTD 9

Db 7 RNDHLLIXD 15

## RESULT 14

A61354  
Carnitine medium/long chain acyltransferase (EC 2.3.1.-) - rat (fragment)  
N/Alternate names: endoplasmic reticulum protein ERp61; glucose regulated protein GRP58;  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999  
C/Accession: A61354  
R/Murthy, M.S.R.; Pande, S.V.  
Mol. Cell. Biochem. 122, 133-138, 1993  
A/Title: Carnitine medium/long chain acyltransferase of microsomes seems to be the previ  
A/Reference number: A61354; MUID:94049728; PMID:8232244  
A/Accession: A61354  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 1-10 <MUR>  
A/Cross-references: UNIPARC:UPI000017C9DE  
C/Keywords: acyltransferase

Query Match 23.0%; Score 17; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 4.4e+03;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 NVLIQTQD 10  
: || ||:  
Db 2 DVLEETDE 9

## RESULT 15

PH0933  
T-cell receptor beta chain V-D-J region (clone 4) - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C/Accession: PH0933  
R/Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A/Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy  
A/Reference number: PH0931; MUID:92078857; PMID:1836012  
A/Accession: PH0933  
A/Molecule type: mRNA  
A/Residues: 1-10 <GOL>  
A/Cross-references: UNIPARC:UPI000017C9E5  
A/Experimental source: complete Freund's adjuvant-immunized lymph node  
A/Note: the authors translated the codon CAG for residue 9 as Glu  
C/Keywords: T-cell receptor

Query Match 23.0%; Score 17; DB 2; Length 10;  
Best Local Similarity 100.0%; Pred. No. 4.4e+03;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNN 3  
: || |  
Db 6 RNN 8

Search completed: May 30, 2006, 10:13:21  
Job time : 13 secs

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 30, 2006, 09:59:07 ; Search time 67.333 Seconds  
(without alignments)  
206.068 Million cell updates/sec

Title: US-10-758-165A-3  
Perfect score: 74  
Sequence: 1 RNNVLIQTDDQATTR 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 8966

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 7.2:\*  
1: uniprotc\_sprot:\*  
2: uniprotc\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	33.8	15	1	NIFS1_ANAVA
2	24	32.4	15	2	Q9S8D5_CYNCA
3	23	31.1	14	2	Q4XS12_PLACH
4	22	29.7	9	2	P70740_RALEU
5	22	29.7	12	2	Q9WZS4_CANFA
6	22	29.7	14	2	Q9TR07_CANFA
7	22	29.7	15	2	Q9TRH1_BOVIN
8	21	28.4	10	2	Q6UDM9_CANFA
9	21	28.4	13	2	Q75MV9_HUMAN
10	21	28.4	14	2	P83330_STRTT
11	21	28.4	15	2	Q29622_STRIT
12	21	28.4	15	2	Q9TR62_RABIT
13	20	27.0	10	1	COX5A_ONCMY
14	20	27.0	10	2	Q9U046_HUMAN
15	20	27.0	15	2	Q6WZ21_HUMAN
16	20	27.0	15	2	Q5GJH2_COXBU
17	20	27.0	15	2	Q5GJH2_COXBU
18	19	25.7	8	2	Q3LVG5_TAROF
19	19	25.7	8	2	Q9SB24_TOBAC
20	19	25.7	10	2	Q53X10_POVBA
21	19	25.7	10	2	Q53X11_POVBA
22	19	25.7	10	2	Q53X12_POVBA
23	19	25.7	10	2	Q53X13_POVBA
24	19	25.7	10	2	Q76V79_9POLY
25	19	25.7	11	1	RANC_RANPI
26	19	25.7	11	2	Q06626_SOLTU
27	19	25.7	11	2	Q5EDJ3_LEGPN
28	19	25.7	13	1	FR12_PEA
29	19	25.7	13	1	Q7M4P7_HUMAN
30	19	25.7	13	2	Q9SB03_ORYSA
31	19	25.7	13	2	Q6RSN3_COXBU

32	19	25.7	14	2	Q9P0W1_HUMAN	Q9P0W1 homo sapien
33	19	25.7	14	2	Q714T6_PSEUK	Q714T6 pyrmesium
34	19	25.7	14	2	Q811Y9_GCYAN	Q811Y9 chirococcid
35	19	25.7	15	1	TX11B_BUNCA	P84471 bungarus ca
36	19	25.7	15	2	Q9UR90_YEAST	Q9UR90 saccharomyc
37	19	25.7	15	2	P82936_HORVU	P82936 hordeum vul
38	19	25.7	15	2	Q8WK21_9STRA	Q8WK21 bolidomonas
39	18	24.3	9	2	Q7M2N7_BOSTA	Q7M2N7 bos indicus
40	18	24.3	9	2	Q4QWV3_9MARC	Q4QWV3 pallavicini
41	18	24.3	9	2	Q4QWV9_9MARC	Q4QWV9 jensenia sp
42	18	24.3	9	2	Q9JH81_HHV8	Q9JH81 retroperito
43	18	24.3	10	1	COCIN_PHACN	P84785 phaeosolus c
44	18	24.3	10	1	CWP14_LYCES	P80810 lycopersico
45	18	24.3	10	2	Q4QWV8_9MARC	Q4QWV8 jensenia di

## ALIGNMENTS

RESULT 1  
NIFS1\_ANAVA STANDARD; PRT; 15 AA.  
ID NIFS1\_ANAVA  
AC Q44507;  
DT 27-APR-2001, integrated into UniProtKB/Swiss-Prot.  
DT 01-NOV-1996, sequence version 1.  
DT 07-FEB-2006, entry version 31.  
DE Cysteine desulfurase 1 (EC 2.8.1.7) (Nitrogenase metalloclusters  
DE biosynthesis protein nifs1) (Fragment).  
GN Name=nifs1; synonym=nifs;  
OS Anabaena variabilis.  
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.  
OX NCBI\_Taxid=1172;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RC STRAIN=PCC 7937 / ATCC 29413;  
RA Monnerjahn U., Boehme H.;  
RU Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP EXPRESSION PATTERN.  
RC STRAIN=PCC 7937 / ATCC 29413;  
RX MEDLINE=96016168; PubMed=7568132;  
RA Thiel T., Lyons E.M., Exler J.C., Ernst A.;  
RT "A second nitrogenase in vegetative cells of a heterocyst-forming  
RT cyanobacterium."  
RT Proc. Natl. Acad. Sci. U.S.A. 92:9358-9362(1995).  
CC -!- FUNCTION: Catalyzes the removal of elemental sulfur atoms from  
CC cysteine to produce alanine. Seems to participate in the  
CC biosynthesis of the nitrogenase metalloclusters by providing the  
CC inorganic sulfur required for the Fe-S core formation (By  
CC similarity).  
CC -!- CATALYTIC ACTIVITY: L-cysteine + [enzyme]-cysteine = L-alanine +  
CC [enzyme]-S-sulfanylcysteine.  
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).  
CC -!- SUBUNIT: Homodimer (By similarity).  
CC -!- MISCELLANEOUS: Belongs to the NifH gene cluster which is expressed  
CC in heterocysts under anaerobic and aerobic conditions.  
CC -!- SIMILARITY: Belongs to the class-V pyridoxal-phosphate-dependent  
CC aminotransferase family. Nifs1/scs subfamily.  
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CC Distributed under the Creative Commons Attribution-NonDerivs license  
CC  
CC EMBL, X69898, CAA49523.1; -, Genomic DNA.  
CC PIR, S32677, S32677.  
DR InterPro: IPR000192; AminoTrans V.  
DR PROSITE: PS00595; AA TRANSFER CLASS 5; PARTIAL.  
KW Nitrogen fixation; Pyridoxal phosphate; Transferrase.  
FT CHAIN 1 >15  
FT Cysteine desulfurase 1.  
FT /FTid=PRO\_0000150248.  
FT  
FT NON\_TER 15  
SQ SEQUENCE 15 AA; 1684 MW; 08B8F106DE5547D CRC64;  
Query Match 33.8%; Score 25; DB 1; Length 15;

Best Local Similarity 45.5%; Pred. No. 1.8e+03;  
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 5 LIQTDQATTR 15  
: |||:  
Db 3 VYLDNNATTK 13

## RESULT 2

ID Q9S8D5\_CYNCA PRELIMINARY; PRT; 15 AA.  
AC Q9S8D5;

DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
DT 01-MAY-2000, sequence version 1.

DT 07-FEB-2006, entry version 11.  
DE CARDOSIN A (Fragment).

OS Cynara cardunculus (Cardoon).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC asterids; campanulids; Asterales; Asteraceae; Carduoideae; Cardueae;

OC Cynara.  
NCBI\_TaxID=4265;

OX NCBI\_TaxID=4265;  
RN [1]

RP PROTEIN SEQUENCE.  
RX MEDLINE=96073661; PubMed=8540346;

RA Faro C., Verissimo P., Lin Y., Tang J., Pires E.;  
"Cardosin A and B, aspartic proteases from the flowers of cardoon.";

RL Adv. Exp. Med. Biol. 362:373-377(1995).  
CC -----

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CC  
SQ SEQUENCE 15 AA; 1555 MW; CC95D9155C97325B CRC64;

Query Match 32.4%; Score 24; DB 2; Length 15;  
Best Local Similarity 36.4%; Pred. No. 2.9e+03;

Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 3 NVLIQTDQAT 13  
: |||:  
Db 4 SAIVATDNQNT 14

## RESULT 3

ID Q4XS12\_PLACH PRELIMINARY; PRT; 14 AA.  
AC Q4XS12;

DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2005, sequence version 1.

DT 07-FEB-2006, entry version 4.  
DE Hypothetical protein (Fragment).

GN ORFNames=PC106890.00.0;  
OS Plasmodium chabaudi.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
NCBI\_TaxID=5825;

OX NCBI\_TaxID=5825;  
RN [1]

RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15637271; DOI=10.1126/science.1103727;

RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,  
Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,  
Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,

RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,  
Karatolos F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,

RA Sinden R.S.;  
"A comprehensive survey of the Plasmodium life cycle by genomic,  
transcriptomic, and proteomic analyses.";

RL Science 307:82-86 (2005).  
CC -----

CC -1- CAUTION: The sequence shown here is derived from an  
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
CC preliminary data.

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CC -----

CC EMBL: CAAJ01003511; CAH80130.1; -; Genomic\_DNA.  
KM Hypothetical protein.

FT NON\_TER 1  
SQ SEQUENCE 14 AA; 1781 MW; 989A795983FA9A51 CRC64;

Query Match 31.1%; Score 23; DB 2; Length 14;  
Best Local Similarity 66.7%; Pred. No. 4.1e+03;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NNVLIQ 7  
: |||:  
Db 8 NNVLIFQ 13

## RESULT 4

ID P70740\_RALEU PRELIMINARY; PRT; 9 AA.  
AC P70740;

DT 01-FEB-1997, integrated into UniProtKB/TrEMBL.  
DT 01-FEB-1997, sequence version 1.

DT 07-FEB-2006, entry version 18.  
DE Hoxa protein (Fragment).

GN Name=hoxa;  
OS Rattus norvegicus (Rat).

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Burkholderiaceae; Cupriavidus.

NCBI\_TaxID=106590;  
OX NCBI\_TaxID=106590;

RN [1]  
RP NUCLEOTIDE SEQUENCE.

RA Lenz O., Schwartz E., Darnedde J., Bittinger M., Friedrich B.;  
"The Alcaigenes eutrophus H16 hoxa gene participates in hydrogenase  
regulation.";

RL J. Bacteriol. 176:4385-4393(1994).  
CC -----

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CC  
DR EMBL: X74670; CAA52736.1; -; Genomic\_DNA.  
FT NON\_TER 9

SQ SEQUENCE 9 AA; 992 MW; 970BD1ADC6D33AB5 CRC64;

Query Match 29.7%; Score 22; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 2.8e+06;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 8 TDQQT 13  
: |||:  
Db 2 SDQQT 7

## RESULT 5

ID G9MZS4\_CANFA PRELIMINARY; PRT; 12 AA.  
AC G9MZS4;

DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.  
DT 01-OCT-2000, sequence version 1.

DT 07-FEB-2006, entry version 8.  
DE Growth hormone (Fragment).

OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
OC Canis.

NCBI\_TaxID=9615;  
OX NCBI\_TaxID=9615;

RN [1]  
RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=22319383; PubMed=12431806; DOI=10.1016/S0303-7207(02)00257-5;  
RA Lantinga-van Leeuwen I.S., Timmermans-Sprang E.A., Mol J.A.;

RA "Cloning and characterization of the 5'-flanking region of the canine  
RT growth hormone gene.";

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CC -----

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RL Biochem Mol. Biol. Int. 29:579-586(1993).
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CC -----
DR GO; GO:0004528; F:phosphodiesterase I activity; IEA.
SQ SEQUENCE 15 AA; 1678 MW; BE31498EEA8B7071 CRC64;

Query Match 29.7%; Score 22; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 6.9e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 4 VLIQTDOQAT 13
DB 2 VLATTMOST 11

RESULT 8
O6JDM9 CANFA
ID Q6JDM9_CANFA PRELIMINARY; PRT; 10 AA.
AC Q6JDM9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Mitochondrial H+ transporting ATP synthase F1 (Fragment).
GN Name=ATP5A1;
OS Canis familiaris (dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15233990; DOI=10.1016/j.ygeno.2004.04.001;
RA Houslay D.J.B., Ritzert E., Vents P.J.;
RT "Comparative radiation hybrid map of canine chromosome 1 (CFA1) incorporating SNP and indel polymorphisms."
RL Genomics 84:248-264(2004).
CC -----
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CC CC -----
DR EMBL; AY514688; AA744872.1; -; Genomic_DNA.
CC CC
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1059 MW; C47457B1A045B042 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 6.7e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 3 NVLIQTDOQ 11
DB 2 NVISITDQ 10

RESULT 9
O7SMV9 HUMAN
ID Q7SMV9_HUMAN PRELIMINARY; PRT; 13 AA.
AC Q7SMV9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 21-FEB-2006, entry version 8.
DE Hypothetical protein SSBP1 (Fragment).
GN Name=SSBP1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;

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RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Powell G.A., Delenauity K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vabnick A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozersky P., Belicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Kolowicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA Tin-Wollam A.-M., Abbott A., Mink P., Maupin R., Strommatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Moesner J.P.,
RA Wendi M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohlmann P.E., Cook L.L.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chisose S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillet W., Zhou Y., James R., Phelps K., Iadamoto S., Bubb K.,
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Frey T.S.,
RA Baertsch R.A., Brent M.R., Keibler E., Flicker P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Wareton R.H., Wilson R.K.,
RT "The DNA sequence of human chromosome 7.";
RL Nature 424:157-164(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Wareton R.;
RN Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
RP [3]
RN NUCLEOTIDE SEQUENCE.
RA Wilson R.;
RN Submitted (JAN-2004) to the EMBL/Genbank/DBJ databases.
CC -----
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CC -----
CC EMBL; AC004979; AAC02037.1; -; Genomic_DNA.
CC KW Hypothetical protein.
CC FT NON TER
SQ SEQUENCE 13 AA; 1565 MW; 9A39BF45040DAB5 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 9.2e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 NVLIQTQD 10
Db 1 NITFLSDQ 8

RESULT 10
P83330_STRTR PRELIMINARY; PRT; 14 AA.
AC P83330;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE M protein, serotype 32 (Fragment).
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=ITCSTR2;
RA Guilmont C., Chopard M.A., Gailard J.L., Chamba J.F.;
RT "Comparative study of the protein composition of three strains of
RT Streptococcus thermophilus grown either in M17 medium or in milk.";
RL Lait 0:0-0(2002).
CC -1- FUNCTION: This protein is one of the different antigenic serotypes
CC of protein M. Protein M is closely associated with virulence of
CC the bacterium and can render the organism resistant to
CC phagocytosis (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Cell wall (By

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CC similarity).
CC -1- SIMILARITY: TO OTHER M PROTEINS.
CC -1- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN
CC THE REGION OF THE MEMBRANE ANCHOR.
CC -----
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CC -----
DR GO; GO:0005618; C:cell wall; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006909; P:phagocytosis; IEA.
KW Antigen; Cell wall; Phagocytosis; Transmembrane; Virulence.
FT NON TER
FT NON TER
SQ SEQUENCE 14 AA; 1739 MW; 66339BF3A3FE24B CRC64;

Query Match 28.4%; Score 21; DB 2; Length 14;
Best Local Similarity 28.6%; Pred. No. 1e+04;
Matches 4; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 2 NVNLIQTQDQARTTR 15
Db 1 NHOULTQENERLTK 14

RESULT 11
Q29622_RABIT PRELIMINARY; PRT; 15 AA.
AC Q29622;
ID Q29622_RABIT PRELIMINARY; PRT; 15 AA.
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 2.
DT 07-FEB-2006, entry version 23.
DE Recombination activating protein (Fragment).
GN Name=RAG-2;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RIM/rqm; TISSUE=Thymus;
RX MEDLINE=93354283; PubMed=8350872; DOI=10.1016/0161-5890(93)90127-W;
RA Fuschioti P., Harindranath N., Mage R.G., McCormack W.T.,
RA Dhanarajan P., Roux K.H.;
RT "Recombination activating genes-1 and -2 of the rabbit: cloning and
RT characterization of germ-line and expressed genes.";
RL Mol. Immunol. 30:1021-1032(1993).
CC -----
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CC -----
CC EMBL; M99310; AAA03028.1; -; mRNA.
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0006310; P:DNA recombination; IEA.
DR InterPro; IPR004321; RAG2.
DR Pfam; PF03089; RAG2; 1.
FT NON TER
FT NON TER
SQ SEQUENCE 15 AA; 1717 MW; CE095FAD5F7ED42B CRC64;

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RNNVLI 6
Db 9 RNNVIAL 14

RESULT 12
Q9TR62_RABIT

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ID 09TR62_RABIT PRELIMINARY; PRT; 15 AA.
AC 09TR62;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE 07-FEB-2006, entry version 9.
DE Apolipoprotein A-IV (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95329112; PubMed=7605356; DOI=10.1016/0021-9150(94)05444-N;
RA Mezdour H., Yamamura T., Nomura S., Yamamoto A.;
RT "Genetic but not diet-induced hypercholesterolemia causes low
RT apolipoprotein A-IV level in rabbit sera.";
RL Atherosclerosis 113:171-178(1995).
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CC
SQ SEQUENCE 15 AA; 1761 MW; DE15B7351F0ABC CRC64;

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 6 IQTDOQT 13
   : |||
Db 2 VSADQVAT 9

RESULT 13
COXS3A ONCMY STANDARD; PRT; 10 AA.
AC P80328;
DT 01-OCT-1994, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1994, sequence version 1.
DT 07-FEB-2006, entry version 27.
DE Cytochrome c oxidase polypeptide Va, mitochondrial (EC 1.9.3.1)
DE (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and Vlla
RT of cytochrome c oxidase isolated from rainbow trout.";
RL Bur. J. Biochem. 221:1111-1116(1994).
CC -1- FUNCTION: This is the heme A-containing chain of cytochrome c
CC oxidase, the terminal oxidase in mitochondrial electron transport.
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner membrane.
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase Va family.
-----
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CC
PIR: S43625; S43625.
KM Direct protein sequencing; Heme; Inner membrane; Iron; Membrane;
KM Metal-binding; Mitochondrion; Oxidoreductase;
FT CHAIN 1 >10 /FTID=PRO_0000195214.
FT NON TER 10 10
SQ SEQUENCE 10 AA; 1144 MW; C535CSB1AB02C33D CRC64;

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Query Match 27.0%; Score 20; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 1.1e+04;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 6 IQTDOQ 11
   : |||
Db 5 VETDEE 10

RESULT 14
O9UJ48_HUMAN PRELIMINARY; PRT; 10 AA.
ID O9UJ48_HUMAN
AC O9UJ48;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Lactophilin-2 (Fragment).
GN Name=LPHN1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99153747; PubMed=10030676; DOI=10.1038/sj.onc.1202487;
RA White G.R.M., Varley J.M., Heighway J.;
RT "Isolation and characterisation of a human homologue of the
RT latrophilin gene from a region of 1p31.1 implicated in breast
RT cancer.";
RL Oncogene 17:3513-3519(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20225451; PubMed=10760572; DOI=10.1016/S0167-4781(00)00020-8;
RA White G.R.M., Varley J.M., Heighway J.;
RT "Genomic structure and expression profile of LPHN1, a 7TM gene
RT variably expressed in breast cancer cell lines.";
RL Biochim. Biophys. Acta 1491:75-92(2000).
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CC
DR EMBL: AJ244514; CAB60206.1; -, Genomic_DNA.
FT NON TER 1 1
SQ SEQUENCE 10 AA; 1112 MW; 06CC4C2720544724 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 NVLIQ 7
   : |||
Db 5 NILIQ 9

RESULT 15
O6MZZ1_HUMAN PRELIMINARY; PRT; 15 AA.
ID O6MZZ1_HUMAN
AC O6MZZ1;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Hypothetical protein DKFZp686J2076.
GN Name=DKFZp686J2076;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human endometrium carcinoma cell line;
RC The German Human cDNA Consortium;

```

RA Ansoorge W., Krieger S., Regiert T., Ritzmuller C., Schwager B.,  
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.,  
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.  
-----  
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>  
CC Distributed under the Creative Commons Attribution-NonCommercial License  
-----  
CC EMBL: BX640801; CAB5884.1; -; mRNA.  
DR Hypothetical protein.  
KW SEQUENCE 15 AA; 1715 MW; 91F5CE0118445CE3 CRC64;  
SQ

Query Match 27.0%; Score 20; DB 2; Length 15;  
Best Local Similarity 42.9%; Pred. No. 1.7e+04;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 LIQTDQ 11  
|:|:  
|:|:  
Db 4 LKVDQE 10

Search completed: May 30, 2006, 11:10:01  
Job time : 69.333 secs





CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC horse IGE 5.91 recognition site.

XX  
 SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RNNVLIQTDQQAATTR 15  
 1 RNNVLIQTDQQAATTR 15  
 Db

RESULT 2

ADC64568  
 ID ADC64568 standard; peptide; 15 AA.

AC ADC64568;

DT 18-DEC-2003 (first entry)

DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide P4.

XX Horse; immunoglobulin E; IGE; heavy chain; immunogen; allergy.

XX Equus caballus.

OS US2003087314-A1.

XX 08-MAY-2003.

XX 08-NOV-2001; 2001US-00052788.

XX 08-NOV-2001; 2001US-00052788.

XX (REGC ) UNIV CALIFORNIA.

XX Gershwin LJ, Pettigrew HD, Kalina WV;

XX WPI; 2003-765437/72.

PT Immunogenic composition comprising an isolated equine immunoglobulin E  
 PT polypeptide that induces production of antibodies which specifically bind  
 PT to equine immunoglobulin E.

XX  
 PS Example 1; Page 8; 14pp; English.

CC The invention relates to an immunogenic composition comprising an  
 CC isolated polypeptide having an amino acid sequence that is at least 80%  
 CC identical to 6 (SI-56), 15 amino acid peptide sequences derived from  
 CC equine immunoglobulin E (the composition induces production of an  
 CC antibody that specifically binds to equine immunoglobulin (Ig)E), the six  
 CC polypeptides are not explicitly identified in the specification. Also  
 CC included are a composition comprising an antibody that specifically binds  
 CC to a polypeptide at least 80% identical to (SI)-(56), an antibody that  
 CC specifically binds to equine IGE made by the process of immunising an  
 CC animal with a polypeptide at least 80% identical to (SI)-(56), making an  
 CC antibody that specifically binds to equine IGE (involving immunising an  
 CC animal with a composition further comprising an isolated polypeptide (the  
 CC amino acid sequence of the polypeptide is at least 80% identical to (SI)-  
 CC (56)), and collecting antiserum from the animal) and a kit for detection  
 CC of equine IGE in a biological sample comprising the antibody and means  
 CC for detecting specific binding of the antibody to equine IGE. The  
 CC antibody is useful for detecting equine IGE protein in a biological  
 CC sample (serum) which involves contacting the sample with the antibody,  
 CC thus forming an antigen/antibody complex, and detecting the presence or  
 CC absence of the antigen/antibody complex. The antibody and antigen are  
 CC immobilised on a solid surface. The antibody is labelled such that the

CC complex can be detected. The complex is detected using a second labelled  
 CC antibody. The peptides are useful for generating antibodies specific for  
 CC IGE which can serve as a diagnostic test for allergy. The present  
 CC sequence is a Horse immunoglobulin E, IGE, heavy chain immunogenic  
 CC peptide from the early portion of the C4 region.

XX  
 SQ Sequence 15 AA;

Query Match 66.2%; Score 49; DB 7; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 0.074;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 IQTDQQAATTR 15  
 1 IQTDQQAATTR 10  
 Db

RESULT 3

ADR10601  
 ID ADR10601 standard; peptide; 15 AA.

AC ADR10601;

DT 21-OCT-2004 (first entry)

DE Dog IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.

XX Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
 XX anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.

XX Canis familiaris.

OS WO2004065936-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.

XX (UNIC-) UNIV NORTH CAROLINA STATE.

XX Hammerberg B;

XX WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IGE epitope, useful  
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
 PT or treating asthma or anaphylactic shock.

XX  
 PS Example 6; Page 9; 14pp; English.

CC The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IGE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the  
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE.

XX  
 SQ Sequence 15 AA;

Query Match 55.4%; Score 41; DB 8; Length 15;  
 Best Local Similarity 64.3%; Pred. No. 2.1;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIQTDQOATT 14  
 ||:|||||  
 DB 1 RNDSPIQTDQYTT 14

## RESULT 4

ID ADR10607 standard; peptide; 15 AA.

AC ADR10607;

DT 21-OCT-2004 (first entry)

DE Pig IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 7.

KM Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;  
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
 pig.

OS Sus scrofa.

PN WO2004065936-A2.

XX 05-AUG-2004.

PF 15-JAN-2004; 2004WO-US003566.

PR 16-JAN-2003; 2003US-0440472P.

PA (UYNC-) UNIV NORTH CAROLINA STATE.

PI Hammerberg B;

DR WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IgE epitope, useful  
 for testing an allergen reactivity of IgE sample, detecting mammalian IgE  
 or treating asthma or anaphylactic shock.

PS Example 6; Page 9; 14pp; English.

CC The present invention relates to a novel monoclonal antibody (I) that  
 specifically binds to a mammalian IgE epitope, where the epitope is  
 between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.  
 CC (I) is useful for testing an allergen reactivity of an IgE sample. The  
 allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 and corn allergens. The sample is a biological sample collected from a  
 dog, cat or horse. (I) is also useful for detecting mammalian IgE and for  
 treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IgE corresponding to amino acid  
 residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the  
 CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from  
 cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE. The present sequence is the  
 CC pig IgE 5.91 recognition site.

XX Sequence 15 AA;

Query Match 54.1%; Score 40; DB 8; Length 15;  
 Best Local Similarity 46.7%; Pred. No. 3.3;  
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLIQTDQOATT 15  
 ||:|||||

DB 1 RNDAPVQADRHSTTR 15

RESULT 5  
 ADR10602  
 ID ADR10602 standard; peptide; 15 AA.

XX ADR10602;

DT 21-OCT-2004 (first entry)

DE Cat IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.

KM Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;  
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
 cat.

OS Felis catus.

PN WO2004065936-A2.

XX 05-AUG-2004.

PF 15-JAN-2004; 2004WO-US003566.

PR 16-JAN-2003; 2003US-0440472P.

PA (UYNC-) UNIV NORTH CAROLINA STATE.

PI Hammerberg B;

DR WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IgE epitope, useful  
 for testing an allergen reactivity of IgE sample, detecting mammalian IgE  
 or treating asthma or anaphylactic shock.

PS Example 6; Page 9; 14pp; English.

CC The present invention relates to a novel monoclonal antibody (I) that  
 specifically binds to a mammalian IgE epitope, where the epitope is  
 between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.  
 CC (I) is useful for testing an allergen reactivity of an IgE sample. The  
 allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 and corn allergens. The sample is a biological sample collected from a  
 dog, cat or horse. (I) is also useful for detecting mammalian IgE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IgE corresponding to amino acid  
 residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the  
 CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 of IgE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IgE. The present sequence is the  
 CC cat IgE 5.91 recognition site.

XX Sequence 15 AA;

Query Match 50.0%; Score 37; DB 8; Length 15;  
 Best Local Similarity 53.8%; Pred. No. 11;  
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 RNNVLIQTDQOATT 14  
 ||:|||||

DB 2 RNDSPVTEQOATT 14

## RESULT 6

ADD44095  
 ID ADD44095 standard; peptide; 15 AA.

AC ADD44095;

DT 15-JAN-2004 (first entry)

DE CPG2 peptide #1 able to stimulate human T-cells in vitro.

KW bacterial enzyme; carboxypeptidase G2; CPG2; non-immunogenic;  
 immunogenic; T-cell epitope; MHC class II binding ligand;

KW immunostimulant; enzyme therapy; immune response;  
 KM gene directed enzyme prodnug strategy; vaccine; enzyme; EC 3.4.17.11.  
 XX  
 OS Pseudomonas sp. RS-16.  
 XX  
 PN WO2003045426-A1.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PP 27-NOV-2002; 2002WO-EP013351.  
 XX  
 PR 29-NOV-2001; 2001EP-00128519.  
 PR 25-JAN-2002; 2002EP-00001778.  
 PR 13-SEP-2002; 2002EP-00020634.  
 XX  
 PA (MERCK ) MERCK PATENT GMBH.  
 XX  
 PI Hellendoorn K, Baker M, Williams S, Carr FJ;  
 DR WPI; 2003-513617/48.  
 XX  
 PT New modified bacterial enzyme carboxypeptidase G2 (CPG2) having  
 PT substantially non-immunogenic or less immunogenic than any non-modified  
 PT CPG2, useful for inducing an immune response in a human host.  
 XX  
 PS Claim 3; Page 14; 52pp; English.  
 XX  
 CC The invention relates to a novel modified bacterial enzyme  
 CC carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2  
 CC proteins that are substantially non-immunogenic or less immunogenic than  
 CC any non-modified CPG2 having essentially the same biological specificity  
 CC when used in vivo, and comprising specific amino acid residues having  
 CC alterations compared with the non-modified parochal enzyme. The  
 CC alterations cause a reduction or an elimination of one or more of T-cell  
 CC epitope sequences, which act in the parental enzyme as MHC class II  
 CC binding ligands and stimulate T-cells. The modified CPG2 enzyme and the  
 CC CPG2 proteins have immunostimulant activity and may be used in enzyme  
 CC therapy. The modified CPG2 enzyme may be used to induce an immune  
 CC response in a human host, or as a therapeutic entity such as the gene  
 CC directed enzyme prodnug strategy. The peptide is useful for the  
 CC manufacture of a modified CPG2 enzyme having substantially no or less  
 CC immunogenicity than any non-modified parental enzyme when used in vivo,  
 CC and for vaccination of patients to reduce immunogenicity to CPG2 in vivo.  
 CC This sequence represents a CPG2 enzyme peptide able to stimulate human T-  
 CC cells in vitro of the invention.  
 CC  
 XX  
 SO Sequence 15 AA;  
 Query Match 43.2%; Score 32; DB 7; Length 15;  
 Best Local Similarity 61.5%; Pred. No. 94;  
 Matches 8; Conservative 2; Mismatches 1; Indels 2; Gaps 1;  
 Oy 1 RNNVLIQ--TDQQ 11  
 | : | | | | | : |  
 3 RDNVLFQATDEQ 15  
 Db  
 RESULT 7  
 ADD44240  
 ID ADD44240 standard; peptide; 15 AA.  
 AC ADD44240;  
 XX  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Carboxypeptidase G2 (CPG2) enzyme immunogenic peptide #1.  
 XX  
 KM bacterial enzyme; carboxypeptidase G2; CPG2; non-immunogenic;  
 KM immunogenic; T-cell epitope; MHC class II binding ligand;  
 KM immunostimulant; enzyme therapy; immune response;  
 KM gene directed enzyme prodnug strategy; vaccine; enzyme; EC 3.4.17.11.  
 XX  
 OS Pseudomonas sp. RS-16.

XX  
 PN WO2003045426-A1.  
 XX  
 PD 05-JUN-2003.  
 XX  
 PF 27-NOV-2002; 2002WO-EP013351.  
 XX  
 PR 29-NOV-2001; 2001EP-00128519.  
 PR 25-JAN-2002; 2002EP-00001778.  
 PR 13-SEP-2002; 2002EP-00020634.  
 XX  
 PA (MERCK ) MERCK PATENT GMBH.  
 XX  
 PI Hellendoorn K, Baker M, Williams S, Carr FJ;  
 DR WPI; 2003-513617/48.  
 XX  
 PT New modified bacterial enzyme carboxypeptidase G2 (CPG2) having  
 PT substantially non-immunogenic or less immunogenic than any non-modified  
 PT CPG2, useful for inducing an immune response in a human host.  
 XX  
 PS Example 2; Fig 1; 52pp; English.  
 XX  
 CC The invention relates to a novel modified bacterial enzyme  
 CC carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2  
 CC proteins that are substantially non-immunogenic or less immunogenic than  
 CC any non-modified CPG2 having essentially the same biological specificity  
 CC when used in vivo, and comprising specific amino acid residues having  
 CC alterations compared with the non-modified parochal enzyme. The  
 CC alterations cause a reduction or an elimination of one or more of T-cell  
 CC epitope sequences, which act in the parental enzyme as MHC class II  
 CC binding ligands and stimulate T-cells. The modified CPG2 enzyme and the  
 CC CPG2 proteins have immunostimulant activity and may be used in enzyme  
 CC therapy. The modified CPG2 enzyme may be used to induce an immune  
 CC response in a human host, or as a therapeutic entity such as the gene  
 CC directed enzyme prodnug strategy. The peptide is useful for the  
 CC manufacture of a modified CPG2 enzyme having substantially no or less  
 CC immunogenicity than any non-modified parental enzyme when used in vivo,  
 CC and for vaccination of patients to reduce immunogenicity to CPG2 in vivo.  
 CC This sequence represents an immunogenic peptide of the CPG2 enzyme of the  
 CC invention.  
 CC  
 XX  
 SO Sequence 15 AA;  
 Query Match 43.2%; Score 32; DB 7; Length 15;  
 Best Local Similarity 61.5%; Pred. No. 94;  
 Matches 8; Conservative 2; Mismatches 1; Indels 2; Gaps 1;  
 Oy 1 RNNVLIQ--TDQQ 11  
 | : | | | | | : |  
 3 RDNVLFQATDEQ 15  
 Db  
 RESULT 8  
 AEC11192  
 ID AEC11192 standard; peptide; 12 AA.  
 AC AEC11192;  
 XX  
 DT 20-OCT-2005 (first entry)  
 XX  
 DE Pseudomonas aeruginosa phosphoglucosamine mutase peptide.  
 XX  
 KM protein purification; antibacterial; antimicrobial; infection;  
 KM drug screening; phosphoglucosamine mutase.  
 XX  
 OS Pseudomonas aeruginosa.  
 XX  
 PN US2005181388-A1.  
 XX  
 PD 18-AUG-2005.  
 XX  
 PF 04-OCT-2004; 2004US-00958216.

XX 02-APR-2002; 2002US-0369511P.  
PR 04-APR-2002; 2002US-0369817P.  
PR 04-APR-2002; 2002US-0370102P.  
PR 08-APR-2002; 2002US-0370778P.  
PR 08-APR-2002; 2002US-0370792P.  
PR 08-APR-2002; 2002US-0370820P.  
PR 08-APR-2002; 2002US-0370859P.  
PR 08-APR-2002; 2002US-0370899P.  
PR 09-APR-2002; 2002US-0371067P.  
PR 09-APR-2002; 2002US-0371107P.  
PR 09-APR-2002; 2002US-0371140P.  
PR 09-APR-2002; 2002US-0371185P.  
PR 31-MAY-2002; 2002US-0385089P.  
PR 31-MAY-2002; 2002US-0385426P.  
PR 04-JUN-2002; 2002US-0385751P.  
PR 05-JUN-2002; 2002US-0386018P.  
PR 05-JUN-2002; 2002US-0386367P.  
PR 05-JUN-2002; 2002US-0386548P.  
PR 05-JUN-2002; 2002US-0386553P.  
PR 05-JUN-2002; 2002US-0386566P.  
PR 05-JUN-2002; 2002US-0386577P.  
PR 06-JUN-2002; 2002US-0386283P.  
PR 06-JUN-2002; 2002US-0386390P.  
PR 06-JUN-2002; 2002US-0386430P.  
PR 06-JUN-2002; 2002US-0386601P.  
PR 06-JUN-2002; 2002US-0386826P.  
PR 06-JUN-2002; 2002US-0386869P.  
PR 31-JUL-2002; 2002US-0399972P.  
PR 01-AUG-2002; 2002US-0400348P.  
PR 05-NOV-2002; 2002US-0421053P.  
PR 06-NOV-2002; 2002US-0424380P.  
PR 08-NOV-2002; 2002US-0425086P.  
PR 08-NOV-2002; 2002US-0425200P.  
PR 24-DEC-2002; 2002US-0436243P.  
PR 24-DEC-2002; 2002US-0436288P.  
PR 24-DEC-2002; 2002US-0436345P.  
PR 24-DEC-2002; 2002US-0436349P.  
PR 26-DEC-2002; 2002US-0436566P.  
PR 26-DEC-2002; 2002US-0436567P.  
PR 26-DEC-2002; 2002US-0436568P.  
PR 27-DEC-2002; 2002US-0436675P.  
PR 27-DEC-2002; 2002US-0436708P.  
PR 27-DEC-2002; 2002US-0436734P.  
PR 27-DEC-2002; 2002US-0436804P.  
PR 27-DEC-2002; 2002US-0436834P.  
PR 27-DEC-2002; 2002US-0436842P.  
PR 27-DEC-2002; 2002US-0436861P.  
PR 27-DEC-2002; 2002US-0436885P.  
PR 27-DEC-2002; 2002US-0436889P.  
PR 27-DEC-2002; 2002US-0436893P.  
PR 27-DEC-2002; 2002US-0436900P.  
PR 30-DEC-2002; 2002US-0436947P.  
PR 30-DEC-2002; 2002US-0436971P.  
PR 30-DEC-2002; 2002US-0436987P.  
PR 30-DEC-2002; 2002US-0437013P.  
PR 30-DEC-2002; 2002US-0437038P.  
PR 30-DEC-2002; 2002US-0437141P.  
PR 31-DEC-2002; 2002US-0437281P.  
PR 31-DEC-2002; 2002US-0437527P.  
PR 31-DEC-2002; 2002US-0437620P.  
PR 31-DEC-2002; 2002US-0437638P.  
PR 02-APR-2003; 2003WO-CA000464.  
PR 04-APR-2003; 2003WO-CA000464.  
PR 08-APR-2003; 2003WO-CA000481.  
PR 08-APR-2003; 2003WO-CA000485.  
XX  
XX (AFFI-) AFFINIUM PHARM INC.  
PA  
XX Edwards A, Dharamsi A, Vedadi M, Arrowsmith C, Awrey DE;  
PI Beattie B, Buzadzija K, Canadien V, Domagala M, Houston S;

PI Kanagaraiah D, Li Q, Mansoury K, McDonald M, Nethery-Brook K, Ng I;  
PI Ouyang H, Pinder B, Richards D, Tai M, Thalakada R, Vallee F;  
PI Vitag C;  
XX WPI, 2005-628189/64.  
DR  
XX  
XX  
PT New composition comprising purified polypeptides from bacteria (e.g.  
PT Escherichia coli), useful for diagnosing, preventing or treating  
PT microbial infections, or in pharmacogenomic or drug screening procedures.  
XX  
XX Example 1; Fig 219; 667pp; English.  
PS  
XX  
XX The invention relates to a composition (I) comprising purified  
CC polypeptides from bacteria. Also described: (1) a crystallized,  
CC recombinant polypeptide comprising an amino acid sequence of (I), where  
CC the polypeptide is in crystal form; (2) a crystallized complex comprising  
CC the crystallized, recombinant polypeptide and a co-factor or a small  
CC organic molecule, where the complex is in crystal form; and (3) a host  
CC cell comprising a nucleic acid encoding a polypeptide of (I), where a  
CC culture of the host cell produces at least about 1 mg of the polypeptide  
CC per liter of culture and the polypeptide is at least about one-third  
CC soluble as measured by gel electrophoresis. The composition and methods  
CC are useful for diagnosing, preventing or treating diseases, such as  
CC microbial infections. These may also be used in pharmacogenomic or drug  
CC screening procedures. The present sequence represents a Pseudomonas  
CC aeruginosa phosphoglucosamine mutase peptide, which is used in an example  
CC from the present invention.  
XX  
XX  
SQ Sequence 12 AA;  
  
Query Match 39.2%; Score 29; DB 9; Length 12;  
Best Local Similarity 33.3%; Pred. No. 2.6e+02;  
Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 4 VLQTPQQAATR 15  
|::|::|:  
Db 1 VMVEGDDEASVR 12  
  
RESULT 9  
AAVE5622  
ID AAVE5622 standard; peptide; 15 AA.  
XX  
AC AAVE5622;  
XX  
DT 01-FEB-2000 (first entry)  
XX  
DE Oestrogen receptor beta ERK binding peptide 175-beta.  
XX  
KM Oestrogen receptor; estrogen; estradiol; oestrogen response element; ERE;  
KM binding; biological activity; fingerprint; molecular biology;  
KM cellular; braille; modulation; tamoxifen; breast cancer; ovarian cancer;  
KM menopause; osteoporosis; selective oestrogen receptor modulator;  
KM identification; characterisation; classification.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
PN WO954728-A2.  
XX  
XX 28-OCT-1999.  
XX  
XX 26-MAR-1999; 99WO-US006664.  
PF  
XX 23-APR-1998; 98US-0082756P.  
PR 09-SEP-1998; 98US-0099656P.  
PR 08-JAN-1999; 99US-0115345P.  
XX  
XX (NOVA-) NOVALON PHARM CORP.  
PA  
XX Paige LA, Hamilton PT, Fowlkes DM, Buehrer B, Barnett T;  
PI McDonnell DP, Christensen DJ;

DR WPI, 2000-013281/01.  
 XX Methods for identifying new receptor modulators, especially estrogen  
 PT modulators to treat tamoxifen refractory breast cancer.  
 PS Example 2.2; Page 164; 219pp; English.  
 XX  
 CC The present invention describes a method for predicting the biological  
 CC activity of new receptor modulating compounds (II) using novel oligomeric  
 CC peptides (biokeys) which have differential abilities to bind to 2  
 CC different receptor conformations. The method is used to identify new  
 CC drugs that are physiological or pharmacological agonists/antagonists and  
 CC that target various receptors, which are involved in certain disease  
 CC conditions. The system may be used as a primary screening tool to  
 CC identify hits, to classify lead compounds from a drug screen to,  
 CC characterize selective oestrogen receptor modulators (SERMs) in terms of  
 CC agonist and antagonist function and to predict possible clinical effects  
 CC of SERMs such as tissue and receptor specificity. The method can also be  
 CC applied to the fractionation of mixtures of SERMs to determine which  
 CC components are producing agonistic and antagonistic activity. The method  
 CC may be used with other receptors (e.g. progesterone, androgen, and  
 CC glucocorticoid, thyroid, vitamin D, beta-adrenergic, dopamine, and  
 CC epidermal growth factor). To identify, characterise and classify  
 CC modulators of receptor activity. Peptides comprising a LXXLL motif may be  
 CC used to modulate the oestrogen receptor in treating e.g. breast and  
 CC ovarian cancer and ameliorating the effects of menopause, including  
 CC osteoporosis. AA65439 to AA65652 represent oestrogen receptor  
 CC estradiol receptor and oestrogen response element binding peptides given  
 CC in the exemplification of the present invention. AA235740 to AA235745  
 CC represent oligonucleotides used in the exemplification of the present  
 CC invention  
 CC  
 XX Sequence 15 AA;  
 SQ  
 Query Match 39.2%; Score 29; DB 3; Length 15;  
 Best Local Similarity 46.2%; Pred. No. 3.3e+02;  
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 OY 3 NVLIQTDOQATTR 15  
 Db 3 NLCLILDQEACSR 15  
 RESULT 10  
 AA06359  
 ID AA06359 standard; peptide; 15 AA.  
 XX  
 AC AA06359;  
 XX  
 DT 21-MAY-2002 (first entry)  
 XX  
 DE Oestrogen receptor beta binding peptide 17E-beta.  
 XX  
 KM Oestrogen receptor; breast cancer; combinatorial peptide library;  
 KM receptor modulating compound.  
 XX  
 OS Synthetic.  
 OS  
 PN WO200204956-A2.  
 XX  
 PD 17-JAN-2002.  
 XX  
 PF 11-JUL-2001; 2001WO-US021867.  
 XX  
 PR 12-JUL-2000; 2000US-00614865.  
 PR 21-MAY-2001; 2001US-00860688.  
 PA (KARO-) KARO BIO USA INC.  
 XX  
 PI Fowlkes DM, Barnett TR, Buehrer B;  
 XX WPI, 2002-154969/20.  
 XX

PT Identifying receptor-binding peptides comprises screening combinatorial  
 PT peptide library presented in form of cells each of which coexpress one  
 PT peptide member and receptor with signal producing system for reporting  
 PT binding.  
 PS Disclosure; Page 146; 175pp; English.  
 XX  
 CC The invention relates to identifying a binding peptide which binds a  
 CC receptor and which is a member of a combinatorial library of peptides,  
 CC comprising screening a combinatorial peptide library presented in the  
 CC form of cells which coexpress the receptor or its ligand-binding receptor  
 CC moiety and one member of the library, together with a signal producing  
 CC system for reporting binding of the peptide to the receptor. Also  
 CC included is a method for predicting the receptor-modulating activity of a  
 CC compound which modulates the biological activity of a receptor comprising  
 CC (a) identifying peptides which bind the receptor by the method above, (b)  
 CC using a number of the peptides to predict the receptor-modulating  
 CC activity of a compound by (i) providing a panel of identified peptides,  
 CC where the members differ in their ability to bind to the receptor  
 CC depending on reference conformations the receptor is in, where the effect  
 CC of a number of reference substances known to modulate the biological  
 CC activity of the receptor on the binding of each member of the panel is  
 CC known and is characterised as a reference fingerprint for each reference  
 CC substance, (ii) screening a test substance of unknown activity relative  
 CC to the receptor to determine its effect on the binding of each member of  
 CC the panel to the receptor, thereby obtaining a test fingerprint for the  
 CC test substance, (iii) comparing the test fingerprint to the reference  
 CC fingerprints and (iv) predicting the biological activity of the test  
 CC substance based on the assumption that its biological activity will be  
 CC similar to that of reference substances with similar fingerprints. The  
 CC method is useful for identifying a binding peptide which binds a  
 CC vertebrate, mammalian, preferably human receptor, an intracellular,  
 CC nuclear, oestrogen or androgen receptor. The identified peptides which  
 CC bind to the receptor are useful for predicting the receptor-modulating  
 CC activity of a compound (e.g. ant/agonists). The receptor-binding library  
 CC members are useful in the prediction of the ability of small organic  
 CC molecules, suitable for pharmaceutical use (e.g. in the case of oestrogen  
 CC receptors, for breast cancer treatment), to interact with the receptor.  
 CC The analyte-binding molecules can also be used for in vivo imaging. The  
 CC method has several advantages over whole animal-based assay systems in  
 CC that the same technology can be applied to a variety of different  
 CC receptors, the system can be used for high throughput screening and  
 CC compound characterisation, and gives very distinct patterns for agonists  
 CC and antagonists of receptor activity using very much less protein. The  
 CC present sequence is an oestrogen receptor binding peptide from a  
 CC combinatorial peptide library  
 CC  
 XX  
 XX Sequence 15 AA;  
 SQ  
 Query Match 39.2%; Score 29; DB 5; Length 15;  
 Best Local Similarity 46.2%; Pred. No. 3.3e+02;  
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 OY 3 NVLIQTDOQATTR 15  
 Db 3 NLCLILDQEACSR 15  
 RESULT 11  
 ADM79070  
 ID ADM79070 standard; peptide; 15 AA.  
 XX  
 AC ADM79070;  
 XX  
 DT 03-JUN-2004 (first entry)  
 XX  
 DE Oestrogen receptor beta binding peptide #57.  
 XX  
 KM binding peptide; drug identification; in vivo imaging;  
 KM oestrogen receptor beta.  
 XX  
 OS Unidentified.  
 OS

PN US2003224390-A1.  
 XX 04-DEC-2003.  
 PD  
 XX  
 PF 17-JAN-2003; 2003US-00346162.  
 XX  
 PR 12-JUL-2000; 2000US-00614865.  
 XX 21-MAY-2001; 2001US-00860688.  
 PR 11-JUL-2001; 2001WO-US021867.  
 XX  
 PA (KARO-) KARO BIO AB.  
 XX  
 PI Fowlkes DM, Barnett TR, Buehrer B;  
 XX WPI; 2004-060539/06.  
 DR  
 XX  
 PT Identifying a binding peptide that binds a receptor, for use as a  
 PT therapeutic or diagnostic agent, comprises screening a combinatorial  
 PT peptide library presented in cells co-expressing a peptide, a receptor  
 PT and a signal producing system.  
 XX  
 PS Example; SEQ ID NO 192; 66pp; English.  
 XX  
 CC The invention relates to a method of identifying a binding peptide which  
 CC binds a receptor comprising screening a combinatorial peptide library  
 CC presented in cells which co-expresses one member peptide and the  
 CC receptor, together with a signal producing system for reporting binding.  
 CC The method is useful in identifying drugs which can mediate the  
 CC biological activity of a target protein. The receptor-binding library  
 CC members may be used as therapeutic or diagnostic reagents, for in vivo  
 CC imaging, or to purify target from a fluid, e.g. blood. The present  
 CC sequence represents an oestrogen receptor beta binding peptide.  
 XX  
 SQ Sequence 15 AA:

Query Match 39.2%; Score 29; DB 8; Length 15;  
 Best Local Similarity 46.2%; Pred. No. 3.3e+02;  
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 NVLIOTDQOATTR 15  
 ||:|:|:|:  
 Db 3 NLTCLLDQDACS 15

RESULT 12  
 ADR10604  
 ID ADR10604 standard; peptide; 15 AA.  
 XX  
 AC ADR10604;  
 XX  
 DT 21-OCT-2004 (first entry)  
 XX  
 DE Sheep IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 4.  
 XX  
 KW Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
 KW sheep.  
 XX  
 OS Ovis aries.  
 OS  
 PN WO2004065936-A2.  
 XX  
 PD 05-AUG-2004.  
 XX  
 PF 15-JAN-2004; 2004WO-US003566.  
 XX  
 PR 16-JAN-2003; 2003US-0440472P.  
 XX  
 PA (UTNC-) UNIV NORTH CAROLINA STATE.  
 XX  
 PI Hammerberg B;  
 XX  
 DR WPI; 2004-593545/57.

XX Novel antibody that specifically binds to mammalian IGE epitope, useful  
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
 PT or treating asthma or anaphylactic shock.  
 PT  
 XX  
 PS Example 6; Page 9; 14pp; English.

CC The present invention relates to a novel monoclonal antibody (1) that  
 CC specifically binds to a mammalian IGE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
 CC (1) is useful for testing an allergen reactivity of an IGE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (1) is also useful for detecting mammalian IGE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the  
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC sheep IGE 5.91 recognition site.

XX Sequence 15 AA:

Query Match 39.2%; Score 29; DB 8; Length 15;  
 Best Local Similarity 40.0%; Pred. No. 3.3e+02;  
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 RNNVLIOTDQOATTR 15  
 ||:|:|:|:  
 Db 1 RNKELMRGCHHTTQ 15

RESULT 13  
 AEC98485  
 ID AEC98485 standard; peptide; 15 AA.  
 XX  
 AC AEC98485;  
 XX  
 DT 01-DEC-2005 (first entry)  
 XX  
 DE HLA-DR binding epitope from HPV E1 protein #185.  
 XX  
 KW Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;  
 KW epitope mapping; immune stimulation; cytotoxic T-lymphocyte;  
 KW human leukocyte antigen.  
 XX  
 OS Human papillomavirus.  
 OS  
 PN WO2005089164-A2.  
 XX  
 PD 29-SEP-2005.  
 XX  
 PF 03-JAN-2005; 2005WO-US000077.  
 XX  
 PR 31-DEC-2003; 2003US-0533211P.  
 PR 02-JUL-2004; 2004US-0584652P.  
 XX  
 PA (EPTM-) EPIMUNE INC.  
 PA (INNO-) INNOGENETICS NV.  
 PA (CHES-) CHESNOT R.  
 PA (NEMW-) NEMMAN M J.  
 PA (MOTH-) MOTHE B.  
 PA (BAKE-) BAKER D.  
 PA (SOUT-) SOUTHWOOD S.  
 PA (BABE-) BABE L M.  
 PA (CHEN-) CHEN Y.  
 PA (DEYO-) DEYOUNG L M.  
 PA (HUAN-) HUANG M T F.  
 PA (POWE-) POWER S D.  
 XX

PI Chesnut R. Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;  
PI Chen Y, Deyoung LM, Huang MTF, Power SD;  
XX WPI; 2005-658982/67.  
XX  
XX New polynucleotide comprises a multi-epitope construct comprising nucleic  
PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte  
PT (CTL) epitopes, useful in preparing a vaccine against HPV.  
XX  
XX Disclosure; Page 325; 518pp; English.  
XX  
XX The invention relates to a new polynucleotide comprising a multi-epitope  
CC construct comprising nucleic acids encoding the human papillomavirus  
CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that  
CC are directly or indirectly joined to one another in the same reading  
CC frame, a vaccine minigene. Also included are a vector comprising the  
CC multi-epitope construct, a polypeptide comprising an amino acid sequence  
CC encoded by the polynucleotide, a composition (comprising the  
CC polynucleotide, vector and/or polypeptide and a carrier), a cell  
CC (comprising the polynucleotide, vector or polypeptide), inducing an  
CC immune response against human papillomavirus virus (HPV) and making the  
CC polynucleotide, vector or polypeptide. The epitopes are derived from  
CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The  
CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the  
CC epitopes in the vaccine protein are disclosed in the tables referred to  
CC in the claims of the specification. The polynucleotide, vector or  
CC polypeptide is useful in preparing a composition for inducing an immune  
CC response against human papillomavirus virus (HPV) and thus providing a  
CC defense against HPV infection and HPV-related cancers. The present  
CC sequence is an HPV-derived peptide epitope that binds to a subclass of  
CC human leukocyte antigen (HLA) peptides.  
XX  
SQ Sequence 15 AA;  
Query Match 37.8%; Score 28; DB 9; Length 15;  
Best Local Similarity 40.0%; Pred. No. 5e+02;  
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
OY 5 LIOTDQOATT 14  
Db 3 MVQVEEQTT 12  
RESULT 14  
AEC98272  
ID AEC98272 standard; peptide; 15 AA.  
XX  
AC AEC98272;  
XX  
XX 01-DEC-2005 (first entry)  
XX  
DE HLA-DR binding epitope from HPV E1 protein #40.  
XX  
KW Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;  
KW epitope mapping; immune stimulation; cytotoxic T-lymphocyte;  
KW human leukocyte antigen.  
XX  
OS Human papillomavirus.  
XX  
PN WO2005089164-A2.  
XX  
PD 29-SEP-2005.  
XX  
PF 03-JAN-2005; 2005WO-US000077.  
XX  
XX 31-DEC-2003; 2003US-053211P.  
PR 02-JUL-2004; 2004US-0584652P.  
XX  
PA (EPIM-) EPIMUNE INC.  
PA (INNO-) INNOGENETICS NV.  
PA (CHES/) CHESNUT R.  
PA (NEWM/) NEWMAN M J.  
PA (MOTH/) MOTHE B.

PA (BAKE/) BAKER D.  
PA (SOUT/) SOUTHWOOD S.  
PA (BABE/) BABE L M.  
PA (CHEN/) CHEN Y.  
PA (DEYO/) DEYOUNG L M.  
PA (HUAN/) HUANG M T F.  
PA (POWE/) POWER S D.  
XX  
PI Chesnut R. Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;  
PI Chen Y, Deyoung LM, Huang MTF, Power SD;  
XX WPI; 2005-658982/67.  
XX  
XX New polynucleotide comprises a multi-epitope construct comprising nucleic  
PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte  
PT (CTL) epitopes, useful in preparing a vaccine against HPV.  
XX  
XX Disclosure; Page 315; 518pp; English.  
XX  
XX The invention relates to a new polynucleotide comprising a multi-epitope  
CC construct comprising nucleic acids encoding the human papillomavirus  
CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that  
CC are directly or indirectly joined to one another in the same reading  
CC frame, a vaccine minigene. Also included are a vector comprising the  
CC multi-epitope construct, a polypeptide comprising an amino acid sequence  
CC encoded by the polynucleotide, a composition (comprising the  
CC polynucleotide, vector and/or polypeptide and a carrier), a cell  
CC (comprising the polynucleotide, vector or polypeptide), inducing an  
CC immune response against human papillomavirus virus (HPV) and making the  
CC polynucleotide, vector or polypeptide. The epitopes are derived from  
CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The  
CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the  
CC epitopes in the vaccine protein are disclosed in the tables referred to  
CC in the claims of the specification. The polynucleotide, vector or  
CC polypeptide is useful in preparing a composition for inducing an immune  
CC response against human papillomavirus virus (HPV) and thus providing a  
CC defense against HPV infection and HPV-related cancers. The present  
CC sequence is an HPV-derived peptide epitope that binds to a subclass of  
CC human leukocyte antigen (HLA) peptides.  
XX  
SQ Sequence 15 AA;  
Query Match 37.8%; Score 28; DB 9; Length 15;  
Best Local Similarity 40.0%; Pred. No. 5e+02;  
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;  
OY 5 LIOTDQOATT 14  
Db 1 MVQVEEQTT 10  
RESULT 15  
AAG95534  
ID AAG95534 standard; peptide; 10 AA.  
XX  
AC AAG95534;  
XX  
XX 18-SEP-2001 (first entry)  
XX  
DE Human complementary peptide, SEQ ID NO: 1728.  
XX  
KW Human; complementary peptide; ligand; drug discovery; drug design.  
XX  
OS Homo sapiens.  
XX  
PN WO200142277-A2.  
XX  
PD 14-JUN-2001.  
XX  
XX 13-DEC-2000; 2000MO-GB004776.  
PR 13-DEC-1999; 99GB-00029464.  
XX



PA (PROT-) PROTEOM LTD.  
 XX  
 PI Roberts GW, Heal JR,  
 XX  
 DR WPI; 2001-408419/43.

XX A set of peptide ligands consisting of specific complementary peptides to  
 PT proteins encoded by genes of the human genome, useful in an assay for  
 PT screening and identifying of one or more novel peptides which are drug  
 PT candidates or pro-drugs.

XX  
 PS Example 4; Page 290; 646pp; English.

XX The invention relates to a set of complementary peptide ligands generated  
 CC from the human genome. The complementary peptides interact with their  
 CC relevant target proteins encoded in the human genome. They can be used as  
 CC reagents in drug discovery and as lead ligands to facilitate drug design  
 CC and development. The present sequence is a complementary peptide provided  
 CC in the specification

XX  
 SQ Sequence 10 AA;

Query Match 36.5%; Score 27; DB 4; Length 10;  
 Best Local Similarity 71.4%; Pred. No. 4.9e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 TDQQT 14  
 :|||  
 Db 1 SDQQT 7 ,

Search completed: May 30, 2006, 10:12:42  
 Job time : 62 secs

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OM protein - protein search, using sw model

Run on: May 30, 2006, 10:21:55 ; Search time 47 Seconds  
(without alignments)  
147.835 Million cell updates/sec

Title: US-10-758-165A-3  
Sequence: 1 RNNVLIOTDQOATTR 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqe, 463214858 residues

Total number of hits satisfying chosen parameters: 395127

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*  
6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	15	US-10-758-165-3	Sequence 3, Appl1
2	49	66.2	15	US-10-052-788-4	Sequence 4, Appl1
3	41	55.4	15	US-10-758-165-1	Sequence 1, Appl1
4	40	54.1	15	US-10-758-165-7	Sequence 7, Appl1
5	37	50.0	15	US-10-758-165-2	Sequence 2, Appl1
6	32	43.2	15	US-10-497-091-128	Sequence 128, App
7	29	39.2	12	US-10-958-216-713	Sequence 713, App
8	29	39.2	15	US-10-346-162-192	Sequence 192, App
9	29	39.2	15	US-10-758-165-4	Sequence 4, Appl1
10	27	36.5	10	US-09-572-404B-1728	Sequence 1728, Ap
11	27	36.5	13	US-10-497-091-14	Sequence 14, Appl
12	27	36.5	14	US-10-172-425B-37	Sequence 37, Appl
13	27	36.5	15	US-10-497-091-129	Sequence 129, Appl
14	26	35.1	12	US-10-935-642-48	Sequence 48, Appl
15	26	35.1	12	US-11-074-477-48	Sequence 15, Appl
16	26	35.1	13	US-10-497-091-15	Sequence 1243, Ap
17	25	33.8	12	US-09-764-868-1243	Sequence 123, App
18	25	33.8	12	US-09-955-999-123	Sequence 123, App
19	25	33.8	14	US-10-221-125-1	Sequence 1, Appl
20	25	33.8	15	US-10-014-340-796	Sequence 796, App
21	25	33.8	15	US-10-225-567A-1123	Sequence 1123, Ap
22	25	33.8	15	US-11-004-270-94	Sequence 94, Appl
23	25	33.8	15	US-11-004-273-94	Sequence 94, Appl
24	24	32.4	9	US-10-117-937-560	Sequence 560, App
25	24	32.4	9	US-10-895-064-2404	Sequence 2404, App
26	24	32.4	9	US-11-067-064-560	Sequence 560, App
27	24	32.4	9	US-11-067-159-560	Sequence 560, App

28	24	32.4	9	6	US-11-129-741-2404	Sequence 2404, App
29	24	32.4	10	4	US-10-117-937-561	Sequence 561, App
30	24	32.4	10	6	US-11-067-064-561	Sequence 561, App
31	24	32.4	10	6	US-11-067-159-561	Sequence 561, App
32	24	32.4	12	4	US-10-097-175-66	Sequence 66, Appl
33	24	32.4	12	4	US-10-264-109-289	Sequence 289, App
34	24	32.4	12	5	US-10-264-109-289	Sequence 289, App
35	24	32.4	13	3	US-09-791-378-584	Sequence 584, App
36	24	32.4	13	3	US-09-791-377-584	Sequence 584, App
37	24	32.4	13	4	US-10-014-340-569	Sequence 569, App
38	24	32.4	13	4	US-10-014-340-569	Sequence 569, App
39	24	32.4	13	4	US-10-014-338-7	Sequence 7, Appl1
40	24	32.4	13	4	US-10-369-736-31	Sequence 31, Appl
41	24	32.4	13	4	US-10-112-582-14	Sequence 14, Appl
42	24	32.4	13	4	US-10-369-738-31	Sequence 31, Appl
43	24	32.4	13	5	US-10-808-187-706	Sequence 706, App
44	24	32.4	13	5	US-10-807-807-706	Sequence 706, App
45	24	32.4	13	6	US-11-028-058-31	Sequence 31, Appl

ALIGNMENTS

```
RESULT 1
US-10-758-165-3
; Sequence 3, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hamnerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-3

Query Match      100.0%  Score 74;  DB 5;  Length 15;
Best Local Similarity 100.0%;  Pred. NO. 2.5e-06;
Matches 15;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

QY      1  RNNVLIOTDQOATTR 15
DB      1  RNNVLIOTDQOATTR 15

RESULT 2
US-10-052-788-4
; Sequence 4, Application US/10052788
; Publication No. US20030087314A1
; GENERAL INFORMATION:
; APPLICANT: Gershwin, Laurel J.
; APPLICANT: Pettigrew, Howard David
; APPLICANT: Kalina, Warren V.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
; FILE REFERENCE: 023070-121000US
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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OTHER INFORMATION: Description of Artificial Sequence:epitope peptide  
OTHER INFORMATION: P4, early portion of C4 of equine IgE epsilon  
OTHER INFORMATION: heavy chain  
US-10-052-788-4

Query Match 66.2%; Score 49; DB 4; Length 15;  
Best Local Similarity 100.0%; Pred. No. 0.078;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 IOTDQOATTR 15  
|||  
Db 1 IOTDQOATTR 10

RESULT 3  
US-10-758-165-1  
; Sequence 1, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Canis familiaris  
US-10-758-165-1

Query Match 55.4%; Score 41; DB 5; Length 15;  
Best Local Similarity 64.3%; Pred. No. 2.2;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 RNNVLIQTDOQATT 14  
|||  
Db 1 RNDSPRIQTQYTTT 14

RESULT 4  
US-10-758-165-7  
; Sequence 7, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Sus scrofa  
US-10-758-165-7

Query Match 54.1%; Score 40; DB 5; Length 15;  
Best Local Similarity 46.7%; Pred. No. 3.3;  
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 RNNVLIQTDOQATTR 15  
|||  
Db 1 RNDAPVQADRHSTR 15

RESULT 5

US-10-758-165-2  
; Sequence 2, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Felis catus  
US-10-758-165-2

Query Match 50.0%; Score 37; DB 5; Length 15;  
Best Local Similarity 53.8%; Pred. No. 11;  
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 NNVLITDQOATT 14  
|||  
Db 2 NDSPVTEQOQATT 14

RESULT 6  
US-10-497-091-128  
; Sequence 128, Application US/10497091  
; Publication No. US20050074863A1  
; GENERAL INFORMATION:  
; APPLICANT: HELLEDOORN, Koen  
; APPLICANT: BAKER, Matthew  
; APPLICANT: WILLIAMS, Steven  
; APPLICANT: CARR, Francis J.  
; TITLE OF INVENTION: T-CELL EPITOPES IN CARBOXYPEPTIDASE G2  
; FILE REFERENCE: MER-130  
; CURRENT APPLICATION NUMBER: US/10/497,091  
; CURRENT FILING DATE: 2004-05-28  
; PRIOR APPLICATION NUMBER: PCT/EP02/13351  
; PRIOR FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: EP02020634.8  
; PRIOR FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: EP02001778.6  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: EP01128519.4  
; PRIOR FILING DATE: 2001-11-29  
; NUMBER OF SEQ ID NOS: 312  
; SOFTWARE: PasteSeq for Windows Version 4.0  
; SEQ ID NO 128  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-497-091-128

Query Match 43.2%; Score 32; DB 5; Length 15;  
Best Local Similarity 61.5%; Pred. No. 90;  
Matches 8; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

OY 1 RNNVLIQ-TDQ 11  
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Db 3 RDNVLFQATDEQ 15

RESULT 7  
US-10-958-216-713  
; Sequence 713, Application US/10958216  
; Publication No. US20050181388A1  
; GENERAL INFORMATION:  
; APPLICANT: EDWARDS, ALED  
; APPLICANT: DHARAMSI, AKIL

```

; APPLICANT: VEDADI, MASOUD
; APPLICANT: ALAM, MUHAMMAD ZAHOR
; APPLICANT: ARROWSMITH, CHERYL
; APPLICANT: AMREY, DONALD E.
; APPLICANT: BEATTIE, BRYAN
; APPLICANT: BUZADZIJ, KRISTINA
; APPLICANT: DOMAGALA, VERONICA
; APPLICANT: DOMAGALA, MEGAN
; APPLICANT: HOUSTON, SIMON
; APPLICANT: KANAGARAJAH, DHUSHY
; APPLICANT: LI, QIN
; APPLICANT: MANSOURY, KAMRAN
; APPLICANT: McDONALD, MERRY-LYNN
; APPLICANT: NETHERY, KATHLEEN
; APPLICANT: NG, IVY
; APPLICANT: OUYANG, HUI
; APPLICANT: PINDER, BENJAMIN
; APPLICANT: RICHARDS, DAWN
; APPLICANT: TAI, MATTHEW
; APPLICANT: THALAKADA, ROSANNE
; APPLICANT: VALLEE, FRANCOIS
; APPLICANT: VIRAG, CRISTINA
; TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM BACTERIA
; FILE REFERENCE: IPT-205.01
; CURRENT APPLICATION NUMBER: US/10/958,216
; CURRENT FILING DATE: 2004-10-04
; PRIOR APPLICATION NUMBER: PCT/CA03/00462
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/369,511
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: 60/385,089
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: 60/385,751
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/386,553
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/386,577
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/386,367
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/386,566
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 60/386,390
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: 60/386,601
; PRIOR FILING DATE: 2002-06-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1132
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 713
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-10-958-216-713

Query Match      39.2% Score 29; DB 5; Length 12;
Best Local Similarity 33.3%; Pred. No. 2.4e+02;
Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY      4 VLIOPTDOQATTR 15
DB      1 VMVGDDEASVR 12

RESULT 8
US-10-346-162-192
; Sequence 192, Application US/10346162
; Publication No. US20030224390A1
; GENERAL INFORMATION:
; APPLICANT: KARO BIO USA, INC.
; APPLICANT: FOWLES, Dana M.
; APPLICANT: BARNETT, Thomas R.
; APPLICANT: BUHRER, Benjamin
```

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; TITLE OF INVENTION: METHOD OF IDENTIFYING CONFORMATION-SENSITIVE BINDING PEPTIDES AND
; FILE REFERENCE: PAGE-1H
; CURRENT APPLICATION NUMBER: US/10/346,162
; CURRENT FILING DATE: 2003-01-17
; PRIOR APPLICATION NUMBER: US 09/614,865
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 09/860,688
; PRIOR FILING DATE: 2001-05-21
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 192
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-346-162-192

Query Match      39.2% Score 29; DB 4; Length 15;
Best Local Similarity 46.2%; Pred. No. 3.1e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      3 NVLIQTDQATTR 15
DB      3 NLCLLDQACSR 15

RESULT 9
US-10-758-165-4
; Sequence 4, Application US/10758165
; Publication No. US20050196616A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Ovis aries
US-10-758-165-4

Query Match      39.2% Score 29; DB 5; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      1 RNNVLIQTDQATTR 15
DB      1 RNKELMRGQHTTQ 15

RESULT 10
US-09-572-404B-1728
; Sequence 1728, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 1728
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
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FEATURE:  
; OTHER INFORMATION: sequence located in TPP2 at 1925-1934 and may interact with Sequ  
; OTHER INFORMATION: 1727 in this patent.  
US-09-572-404B-1728

Query Match 36.5%; Score 27; DB 3; Length 10;  
Best Local Similarity 71.4%; Pred. No. 4.5e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 TDQOATT 14  
: ||| :  
Db 1 SDQOTT 7

RESULT 11  
US-10-497-091-14  
; Sequence 14, Application US/10497091  
; Publication No. US20050074863A1  
; GENERAL INFORMATION:  
; APPLICANT: HELLEDOORN, Koen  
; APPLICANT: BAKER, Matthew  
; APPLICANT: WILLIAMS, Steven  
; APPLICANT: CARR, Francis J.  
; TITLE OF INVENTION: T-CELL EPITOPES IN CARBOXYPEPTIDASE G2  
; FILE REFERENCE: MER-130  
; CURRENT APPLICATION NUMBER: US/10/497,091  
; CURRENT FILING DATE: 2004-05-28  
; PRIOR APPLICATION NUMBER: PCT/EP02/13351  
; PRIOR FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: EP02020634.8  
; PRIOR FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: EP02001778.6  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: EP01128519.4  
; PRIOR FILING DATE: 2001-11-29  
; NUMBER OF SEQ ID NOS: 312  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-497-091-14

Query Match 36.5%; Score 27; DB 5; Length 13;  
Best Local Similarity 58.3%; Pred. No. 6.1e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

OY 2 NNVLIO--TDQO 11  
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Db 1 DNVLFOAATDEQ 12

RESULT 12  
US-10-172-425B-37  
; Sequence 37, Application US/10172425B  
; Publication No. US20030147908A1  
; GENERAL INFORMATION:  
; APPLICANT: Kaempfer, Raymond  
; APPLICANT: Ared, Gila  
; TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES  
; FILE REFERENCE: A31967-PCT-USA-A-066031.0164  
; CURRENT APPLICATION NUMBER: US/10/172,425B  
; CURRENT FILING DATE: 2002-06-13  
; PRIOR APPLICATION NUMBER: 09/150,947  
; PRIOR FILING DATE: 1998-09-10  
; PRIOR APPLICATION NUMBER: PCT/IL97/00438  
; PRIOR FILING DATE: 1997-12-30  
; PRIOR APPLICATION NUMBER: ISRAEL 119938  
; PRIOR FILING DATE: 1996-12-30  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 37

LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-10-172-425B-37

Query Match 36.5%; Score 27; DB 4; Length 14;  
Best Local Similarity 44.4%; Pred. No. 6.6e+02;  
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 6 IOTDQATT 14  
: ||| :  
Db 1 VOTDKSVT 9

RESULT 13  
US-10-497-091-129  
; Sequence 129, Application US/10497091  
; Publication No. US20050074863A1  
; GENERAL INFORMATION:  
; APPLICANT: HELLEDOORN, Koen  
; APPLICANT: BAKER, Matthew  
; APPLICANT: WILLIAMS, Steven  
; APPLICANT: CARR, Francis J.  
; TITLE OF INVENTION: T-CELL EPITOPES IN CARBOXYPEPTIDASE G2  
; FILE REFERENCE: MER-130  
; CURRENT APPLICATION NUMBER: US/10/497,091  
; CURRENT FILING DATE: 2004-05-28  
; PRIOR APPLICATION NUMBER: PCT/EP02/13351  
; PRIOR FILING DATE: 2002-11-27  
; PRIOR APPLICATION NUMBER: EP02020634.8  
; PRIOR FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: EP02001778.6  
; PRIOR FILING DATE: 2002-01-25  
; PRIOR APPLICATION NUMBER: EP01128519.4  
; PRIOR FILING DATE: 2001-11-29  
; NUMBER OF SEQ ID NOS: 312  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 129  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-497-091-129

Query Match 36.5%; Score 27; DB 5; Length 15;  
Best Local Similarity 58.3%; Pred. No. 7.2e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

OY 2 NNVLIO--TDQO 11  
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Db 1 DNVLFOAATDEQ 12

RESULT 14  
US-10-935-642-48  
; Sequence 48, Application US/10935642  
; Publication No. US20050050656A1  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Xueying  
; APPLICANT: Wang, Hong  
; TITLE OF INVENTION: Peptide-Based Conditioners and Colorants for Hair, Skin, and  
; FILE REFERENCE: CL2296 US NA  
; CURRENT APPLICATION NUMBER: US/10/935,642  
; CURRENT FILING DATE: 2004-09-07  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 48  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Hair-binding peptide

US-10-935-642-48

Query Match 35.1%; Score 26; DB 5; Length 12;  
Best Local Similarity 62.5%; Pred. No. 8.4e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 TDQOATR 15  
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1 TDMQAPTK 8

RESULT 15

US-11-074-473-48

; Sequence 48, Application US/11074473  
; Publication No. US20050226839A1  
; GENERAL INFORMATION:  
; APPLICANT: Huang, Xueying  
; APPLICANT: Wang, Hong  
; APPLICANT: Mu, Ying  
; TITLE OF INVENTION: Peptide-Based Conditioners and Colorants for Hair, Skin, and  
; TITLE OF INVENTION: Nail  
; FILE REFERENCE: CL2296 US NA  
; CURRENT APPLICATION NUMBER: US/11/074,473  
; CURRENT FILING DATE: 2005-03-08  
; PRIOR APPLICATION NUMBER: US/10/935,642  
; PRIOR FILING DATE: 2004-09-07  
; NUMBER OF SEQ ID NOS: 104  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 48  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Hair-binding peptide  
US-11-074-473-48

Query Match 35.1%; Score 26; DB 6; Length 12;  
Best Local Similarity 62.5%; Pred. No. 8.4e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 TDQOATR 15  
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1 TDMQAPTK 8

Search completed: May 30, 2006, 10:24:41  
Job time : 47 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 30, 2006, 10:22:25 ; Search time 5.66667 Seconds  
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29.481 Million cell updates/sec

Title: US-10-758-165A-3  
Perfect score: 74  
Sequence: 1 RNNVLIOTDQQTTR 15

Scoring table:  
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Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 1113735 residues

Total number of hits satisfying chosen parameters: 10973

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA New:\*  
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2: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US06\_NEW\_PUB pep:\*  
3: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US07\_NEW\_PUB pep:\*  
4: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US08\_NEW\_PUB pep:\*  
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6: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US10\_NEW\_PUB pep:\*  
7: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US11\_NEW\_PUB pep:\*  
8: /EMC\_Celerra\_SIDS3/ptodata/1/pubpaa/US60\_NEW\_PUB pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	35.1	10	US-10-516-079-64	Sequence 64, Appl
2	22	29.7	9	US-10-516-079-94	Sequence 94, Appl
3	22	29.7	14	US-11-118-524-5	Sequence 5, Appl
4	21	28.4	9	US-10-516-079-90	Sequence 90, Appl
5	20	27.0	6	US-10-538-066-625	Sequence 625, Appl
6	20	27.0	11	US-10-538-066-4	Sequence 4, Appl
7	20	27.0	14	US-11-176-182-52	Sequence 52, Appl
8	19	25.7	9	US-10-538-066-159	Sequence 159, Appl
9	19	25.7	9	US-10-473-691B-7	Sequence 7, Appl
10	19	25.7	10	US-11-140-487A-1987	Sequence 1987, Appl
11	19	25.7	12	US-11-176-182-112	Sequence 112, Appl
12	19	25.7	13	US-11-176-182-17	Sequence 17, Appl
13	19	25.7	13	US-11-122-986-822	Sequence 822, Appl
14	19	25.7	15	US-11-140-487A-2124	Sequence 2124, Appl
15	19	25.7	15	US-11-140-487A-2125	Sequence 2125, Appl
16	19	25.7	7	US-11-140-487A-2240	Sequence 2240, Appl
17	19	25.7	15	US-11-140-487A-2241	Sequence 2241, Appl
18	19	24.3	4	US-10-543-587-43	Sequence 43, Appl
19	18	24.3	9	US-10-538-066-65	Sequence 65, Appl
20	18	24.3	9	US-10-538-066-66	Sequence 66, Appl
21	18	24.3	9	US-11-140-487A-343	Sequence 343, Appl
22	18	24.3	9	US-11-140-487A-437	Sequence 437, Appl
23	18	24.3	9	US-11-140-487A-546	Sequence 546, Appl
24	18	24.3	9	US-11-140-487A-1988	Sequence 1988, Appl
25	18	24.3	10	US-10-538-066-267	Sequence 267, Appl

26	18	24.3	10	6	US-10-538-066-268	Sequence 268, Appl
27	18	24.3	10	6	US-10-538-066-574	Sequence 574, Appl
28	18	24.3	10	7	US-11-140-487A-994	Sequence 994, Appl
29	18	24.3	10	7	US-11-140-487A-1989	Sequence 1989, Appl
30	18	24.3	11	6	US-10-538-066-479	Sequence 479, Appl
31	18	24.3	11	6	US-10-538-066-636	Sequence 636, Appl
32	18	24.3	12	7	US-11-122-986-570	Sequence 570, Appl
33	18	24.3	15	6	US-10-516-263-6	Sequence 6, Appl
34	18	24.3	15	6	US-11-122-986-725	Sequence 725, Appl
35	17	23.0	4	7	US-11-252-276-62	Sequence 62, Appl
36	17	23.0	8	7	US-11-122-986-30	Sequence 30, Appl
37	17	23.0	9	6	US-10-516-079-91	Sequence 91, Appl
38	17	23.0	9	7	US-11-122-986-263	Sequence 263, Appl
39	17	23.0	10	6	US-10-538-066-240	Sequence 240, Appl
40	17	23.0	10	6	US-10-538-066-655	Sequence 655, Appl
41	17	23.0	11	7	US-11-122-986-655	Sequence 655, Appl
42	17	23.0	13	7	US-11-298-718-44	Sequence 44, Appl
43	17	23.0	13	7	US-11-142-051-12	Sequence 12, Appl
44	17	23.0	14	7	US-11-176-182-63	Sequence 63, Appl
45	17	23.0	14	7	US-11-176-182-114	Sequence 114, Appl

## ALIGNMENTS

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RESULT 1
US-10-516-079-64
; Sequence 64, Application US/10516079
; Publication No. US20060088899A1
; GENERAL INFORMATION:
; APPLICANT: ALVAREZ, Vernon L.
; APPLICANT: GRIMES, Carol A.
; TITLE OF INVENTION: Combination chemotherapy with chlorotoxin
; FILE REFERENCE: 51530-5006-WO
; CURRENT APPLICATION NUMBER: US/10/516,079
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: US 60/406,033
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/384,171
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Pep21-SCX8_LEIGH sequence
US-10-516-079-64

Query Match      35.1% Score 26; DB 6; Length 10;
Best Local Similarity 62.5% Pred. No. 12;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      8 TDQQTTR 15
      |||||:
Db      2 TDQQTTR 9

RESULT 2
US-10-516-079-94
; Sequence 94, Application US/10516079
; Publication No. US20060088899A1
; GENERAL INFORMATION:
; APPLICANT: ALVAREZ, Vernon L.
; APPLICANT: GRIMES, Carol A.
; APPLICANT: GONDA, Matthew A.
; TITLE OF INVENTION: Combination chemotherapy with chlorotoxin
; FILE REFERENCE: 51530-5006-WO
; CURRENT APPLICATION NUMBER: US/10/516,079
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: US 60/406,033
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PRIOR FILING DATE: 2002-08-27  
PRIOR APPLICATION NUMBER: US 60/384,171  
PRIOR FILING DATE: 2002-05-31  
NUMBER OF SEQ ID NOS: 95  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 94  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Mesobuthus tamulus sindicus  
FEATURE:  
OTHER INFORMATION: GenBank Accession No. F15229, small toxin  
US-10-516-079-94

Query Match 29.7%; Score 22; DB 6; Length 9;  
Best Local Similarity 50.0%; Pred. No. 5.2e+04;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 TDQOATTR 15  
||| : :  
Db 2 TDQOMSKK 9

RESULT 3  
US-11-118-524-5  
Sequence 5, Application US/11118524  
Publication No. US20060088847A1  
GENERAL INFORMATION:  
APPLICANT: GU, WEI  
TITLE OF INVENTION: ARF-BP1 AS MEDIATOR OF P53-DEPENDENT AND INDEPENDENT TUMOR  
FILE REFERENCE: 19240-497US2  
CURRENT APPLICATION NUMBER: US/11/118,524  
CURRENT FILING DATE: 2005-04-29  
PRIOR APPLICATION NUMBER: 60/610,506  
PRIOR FILING DATE: 2004-09-15  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 5  
LENGTH: 14  
TYPE: PRT  
ORGANISM: homo sapiens  
US-11-118-524-5

Query Match 29.7%; Score 22; DB 7; Length 14;  
Best Local Similarity 80.0%; Pred. No. 1.1e+02;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TDQQA 12  
||| :  
Db 2 TDQEA 6

RESULT 4  
US-10-516-079-90  
Sequence 90, Application US/10516079  
Publication No. US20060088899A1  
GENERAL INFORMATION:  
APPLICANT: ALVAREZ, Vernon L.  
APPLICANT: GRIMES, Carol A.  
APPLICANT: GONDA, Matthew A.  
TITLE OF INVENTION: Combination chemotherapy with chlorotoxin  
FILE REFERENCE: 51530-5006-WO  
CURRENT APPLICATION NUMBER: US/10/516,079  
CURRENT FILING DATE: 2004-11-29  
PRIOR APPLICATION NUMBER: US 60/406,033  
PRIOR FILING DATE: 2002-08-27  
PRIOR APPLICATION NUMBER: US 60/384,171  
PRIOR FILING DATE: 2002-05-31  
NUMBER OF SEQ ID NOS: 95  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 90  
LENGTH: 9  
TYPE: PRT

ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Peptide 21a-A5 sequence  
US-10-516-079-90

Query Match 28.4%; Score 21; DB 6; Length 9;  
Best Local Similarity 50.0%; Pred. No. 5.2e+04;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 TDQOATTR 15  
||| :  
Db 1 TDHQARK 8

RESULT 5  
US-10-538-066-625  
Sequence 625, Application US/10538066  
Publication No. US20060094649A1  
GENERAL INFORMATION:  
APPLICANT: Epiimmune Inc.  
TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen  
FILE REFERENCE: 2060.015PC06  
CURRENT APPLICATION NUMBER: US/10/538,066  
CURRENT FILING DATE: 2005-06-09  
PRIOR APPLICATION NUMBER: US 60/432,017  
PRIOR FILING DATE: 2002-12-10  
NUMBER OF SEQ ID NOS: 767  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 625  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-538-066-625

Query Match 27.0%; Score 20; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.2e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NNVL 5  
||| :  
Db 3 NNVL 6

RESULT 6  
US-10-538-066-4  
Sequence 4, Application US/10538066  
Publication No. US20060094649A1  
GENERAL INFORMATION:  
APPLICANT: Epiimmune Inc.  
TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen  
FILE REFERENCE: 2060.015PC06  
CURRENT APPLICATION NUMBER: US/10/538,066  
CURRENT FILING DATE: 2005-06-09  
PRIOR APPLICATION NUMBER: US 60/432,017  
PRIOR FILING DATE: 2002-12-10  
NUMBER OF SEQ ID NOS: 767  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 4  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-538-066-4

Query Match 27.0%; Score 20; DB 6; Length 11;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NNVL 5  
||| :  
Db 5 NNVL 8

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RESULT 7
US-11-176-182-52
; Sequence 52, Application US/11176182
; Publication No. US20060088549A1
; GENERAL INFORMATION:
; APPLICANT: ARNOLD, EDWARD
; TITLE OF INVENTION: PERSTANDIG ARNOLD, GAIL
; FILE REFERENCE: PA04-701-S
; CURRENT APPLICATION NUMBER: US/11/176,182
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52
; LENGTH: 14
; TYPE: PRT
; ORGANISM: chimeric HIV-HRV
US-11-176-182-52

Query Match          27.0%; Score 20; DB 7; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      7 QTPDOATT 14
      :|::|
      4 ELDRKWT 11

Db

RESULT 8
US-10-538-066-159
; Sequence 159, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 159
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-159

Query Match          25.7%; Score 19; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.2e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 QOAT 13
      :|::|
      1 QOAT 4

Db

RESULT 9
US-10-473-691B-7
; Sequence 7, Application US/10473691B
; Publication No. US2006009202A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: IMMUNOLOGUIN CONSTRUCT CONTAINING TUMOR SPECIFIC P53BP2 SEQUENC
; FILE REFERENCE: 02755/100K313-US1
; CURRENT APPLICATION NUMBER: US/10/473,691B
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: PCT/US02/10224
; PRIOR FILING DATE: 2002-04-01
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; PRIOR APPLICATION NUMBER: US 60/280,733
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P52 BP2
US-10-473-691B-7

Query Match          25.7%; Score 19; DB 6; Length 9;
Best Local Similarity 28.6%; Pred. No. 5.2e+04;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      5 LIQTDQ 11
      :|::|
      2 LVETKE 8

Db

RESULT 10
US-11-140-487A-1987
; Sequence 1987, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1987
; LENGTH: 10
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-1987

Query Match          25.7%; Score 19; DB 7; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      4 VLIQTDQAT 13
      :|::|
      1 VVVAIDALMT 10

Db

RESULT 11
US-11-176-182-112
; Sequence 112, Application US/11176182
; Publication No. US20060088549A1
; GENERAL INFORMATION:
; APPLICANT: ARNOLD, EDWARD
; TITLE OF INVENTION: PERSTANDIG ARNOLD, GAIL
; FILE REFERENCE: PA04-701-S
; CURRENT APPLICATION NUMBER: US/11/176,182
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.3
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SEQ ID NO 112  
LENGTH: 12  
TYPE: PRT  
ORGANISM: chimeric HIV-HRV  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (12)-(12)  
OTHER INFORMATION: Xaa can be any naturally occurring amino acid  
US-11-176-182-112

Query Match 25.7%; Score 19; DB 7; Length 12;  
Best Local Similarity 33.3%; Pred. No. 3.5e+02;  
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IQTDOQATT 14  
::|::|:  
Db 2 VELDKMAST 10

RESULT 12

US-11-176-182-17  
Sequence 17, Application US/11176182  
Publication No. US20060088549A1  
GENERAL INFORMATION:  
APPLICANT: ARNOLD, EDWARD  
TITLE OF INVENTION: CHIMERIC HIV VACCINE  
FILE REFERENCE: PA04-701-S  
CURRENT APPLICATION NUMBER: US/11/176,182  
CURRENT FILING DATE: 2005-07-07  
NUMBER OF SEQ ID NOS: 138  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 17  
LENGTH: 13  
TYPE: PRT  
ORGANISM: chimeric HIV-HRV  
US-11-176-182-17

Query Match 25.7%; Score 19; DB 7; Length 13;  
Best Local Similarity 33.3%; Pred. No. 3.8e+02;  
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 6 IQTDOQATT 14  
::|::|:  
Db 3 VELDKMAST 11

RESULT 13

US-11-122-986-822  
Sequence 822, Application US/11122986  
Publication No. US20060104989A1  
GENERAL INFORMATION:  
APPLICANT: EDWARDS, ALED  
APPLICANT: DHARMSI, AKIL  
APPLICANT: VEDADI, MASOUD  
TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES  
FILE REFERENCE: IPR-330.01  
CURRENT APPLICATION NUMBER: US/11/122,986  
CURRENT FILING DATE: 2005-05-05  
PRIOR APPLICATION NUMBER: 60/423,875  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: 60/423,832  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: 60/423,915  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: 60/423,757  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: 60/423,758  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: 60/424,367  
PRIOR FILING DATE: 2002-11-06  
PRIOR APPLICATION NUMBER: 60/424,376  
PRIOR FILING DATE: 2002-11-06

PRIOR APPLICATION NUMBER: 60/424,370  
PRIOR FILING DATE: 2002-11-06  
PRIOR APPLICATION NUMBER: 60/424,362  
PRIOR FILING DATE: 2002-11-06  
PRIOR APPLICATION NUMBER: 60/424,373  
PRIOR FILING DATE: 2002-11-06  
Remaining Prior Application data removed - See file wrapper or PALM.  
NUMBER OF SEQ ID NOS: 844  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 822  
LENGTH: 13  
TYPE: PRT  
ORGANISM: Enterococcus faecalis  
US-11-122-986-822

Query Match 25.7%; Score 19; DB 7; Length 13;  
Best Local Similarity 40.0%; Pred. No. 3.8e+02;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 6 IQTDOQATT 15  
|::|:  
Db 4 INTVOELTNK 13

RESULT 14

US-11-140-487A-2124  
Sequence 2124, Application US/11140487A  
Publication No. US20060093617A1  
GENERAL INFORMATION:  
APPLICANT: Immunogenetics N.V.  
TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi  
FILE REFERENCE: 166  
CURRENT APPLICATION NUMBER: US/11/140,487A  
CURRENT FILING DATE: 2005-05-31  
PRIOR APPLICATION NUMBER: EP 04012951.2  
PRIOR FILING DATE: 2004-06-01  
PRIOR APPLICATION NUMBER: EP 04447239.7  
PRIOR FILING DATE: 2004-10-28  
PRIOR APPLICATION NUMBER: EP 05102441.2  
PRIOR FILING DATE: 2005-03-25  
PRIOR APPLICATION NUMBER: US 60/576,310  
PRIOR FILING DATE: 2004-06-03  
PRIOR APPLICATION NUMBER: US 60/622,782  
PRIOR FILING DATE: 2004-10-29  
PRIOR APPLICATION NUMBER: US 60/665,395  
PRIOR FILING DATE: 2005-03-25  
NUMBER OF SEQ ID NOS: 2278  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2124  
LENGTH: 15  
TYPE: PRT  
ORGANISM: hepatitis C virus  
US-11-140-487A-2124

Query Match 25.7%; Score 19; DB 7; Length 15;  
Best Local Similarity 40.0%; Pred. No. 4.5e+02;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 VLIOTDOQAT 13  
::|::|:  
Db 3 VVAVTDLMT 12

RESULT 15

US-11-140-487A-2125  
Sequence 2125, Application US/11140487A  
Publication No. US20060093617A1  
GENERAL INFORMATION:  
APPLICANT: Immunogenetics N.V.  
TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi  
FILE REFERENCE: 166  
CURRENT APPLICATION NUMBER: US/11/140,487A  
CURRENT FILING DATE: 2005-05-31

; PRIOR APPLICATION NUMBER: EP 04012951.2  
; PRIOR FILING DATE: 2004-06-01  
; PRIOR APPLICATION NUMBER: EP 04447239.7  
; PRIOR FILING DATE: 2004-10-28  
; PRIOR APPLICATION NUMBER: EP 05102441.2  
; PRIOR FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: US 60/576,310  
; PRIOR FILING DATE: 2004-06-03  
; PRIOR APPLICATION NUMBER: US 60/622,782  
; PRIOR FILING DATE: 2004-10-29  
; PRIOR APPLICATION NUMBER: US 60/665,395  
; PRIOR FILING DATE: 2005-03-25  
; NUMBER OF SEQ ID NOS: 2278  
; SOFTWARE: Patent version 3.1  
; SEQ ID NO 2125  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: hepatitis C virus  
US-11-140-487A-2125

Query Match 25.7%; Score 19; DB 7; Length 15;  
Best Local Similarity 40.0%; Pred. No. 4.5e+02;  
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 VLIOTDQAT 13  
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Db 3 VVATDALT 12

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Job time : 6.66667 secs

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Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2006, 09:59:16 ; Search time 20.3333 Seconds  
(without alignments)  
64.572 Million cell updates/sec

Title: US-10-758-165A-2  
Perfect score: 85  
Sequence: 1 HNDSPVTEQQATTW 15

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Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 249102

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /EMC\_Celerra\_SIDS3/prodata/2/iaa/6.COMB.pep.\*  
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6: /EMC\_Celerra\_SIDS3/prodata/2/iaa/RE.COMB.pep.\*  
7: /EMC\_Celerra\_SIDS3/prodata/2/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	35.3	10	2	US-09-526-193A-65 Sequence 65, Appl
2	28.5	33.5	12	2	US-08-851-567B-2 Sequence 2, Appl
3	28	32.9	9	2	US-09-339-922A-88 Sequence 88, Appl
4	28	32.9	9	2	US-09-016-061-88 Sequence 88, Appl
5	28	32.9	13	7	5223254-6 Patent No. 5223254
6	28	32.9	15	3	US-09-641-528B-48206 Sequence 48206, A
7	27	31.8	13	2	US-08-836-075A-166 Sequence 166, App
8	27	31.8	13	2	US-08-878-281A-244 Sequence 244, App
9	27	31.8	13	2	US-09-851-158C-166 Sequence 166, App
10	27	31.8	14	3	US-10-000-986A-144 Sequence 144, App
11	27	31.8	15	5	PCT-US95-04018-56 Sequence 56, Appl
12	27	31.8	15	5	PCT-US95-04018-56 Sequence 56, Appl
13	26	30.6	9	3	US-09-641-528B-49922 Sequence 49922, Ap
14	26	30.6	9	3	US-09-641-528B-13784 Sequence 13784, A
15	26	30.6	9	3	US-09-641-528B-26852 Sequence 26852, A
16	26	30.6	9	3	US-09-641-528B-45697 Sequence 45697, A
17	26	30.6	9	3	US-09-641-528B-49305 Sequence 49305, A
18	26	30.6	9	3	US-09-641-528B-49332 Sequence 49332, A
19	26	30.6	9	3	US-09-641-528B-50984 Sequence 50984, A
20	26	30.6	10	2	US-08-981-382-53 Sequence 53, Appl
21	26	30.6	10	2	US-09-620-031-436 Sequence 436, App
22	26	30.6	10	2	US-09-908-322-53 Sequence 53, Appl
23	26	30.6	10	3	US-09-641-528B-804 Sequence 804, App
24	26	30.6	10	3	US-09-641-528B-4809 Sequence 4809, Ap
25	26	30.6	10	3	US-09-641-528B-4923 Sequence 4923, Ap
26	26	30.6	10	3	US-09-641-528B-4987 Sequence 4987, Ap

ALIGNMENTS

27	26	30.6	10	3	US-09-641-428B-13808 Sequence 13808, A
28	26	30.6	10	3	US-09-641-428B-26799 Sequence 26799, A
29	26	30.6	11	3	US-09-641-528B-26913 Sequence 26913, A
30	26	30.6	11	3	US-09-641-528B-4810 Sequence 4810, Ap
31	26	30.6	11	3	US-09-641-528B-4856 Sequence 4856, Ap
32	26	30.6	11	3	US-09-641-528B-13626 Sequence 13626, A
33	26	30.6	11	3	US-09-641-528B-13785 Sequence 13785, A
34	26	30.6	11	3	US-09-641-528B-26703 Sequence 26703, A
35	26	30.6	11	3	US-09-641-528B-26893 Sequence 26893, A
36	26	30.6	11	3	US-09-641-528B-34845 Sequence 34845, A
37	26	30.6	11	3	US-09-641-528B-42043 Sequence 42043, A
38	26	30.6	12	2	US-09-641-528B-45698 Sequence 45698, A
39	26	30.6	12	2	US-09-620-091-172 Sequence 172, App
40	26	30.6	14	1	US-08-937-941-28 Sequence 28, Appl
41	26	30.6	14	1	US-08-937-941-28 Sequence 28, Appl
42	26	30.6	15	2	US-09-148-712-23 Sequence 23, Appl
43	26	30.6	15	2	US-09-535-364-10 Sequence 10, Appl
44	26	30.6	15	3	US-09-641-528B-47147 Sequence 47147, A
45	26	30.6	15	3	US-09-641-528B-47208 Sequence 47208, A

```
RESULT 1
US-09-526-193A-65
; Sequence 65, Application US/09526193A
; Patent No. 6617122
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING
; FILE REFERENCE: 50110/002005
; CURRENT APPLICATION NUMBER: US/09/526, 193A
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-526-193A-65

Query Match      35.3%; Score 30; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 NDSFVTEQQ 11
      || || || ||
Db      1 NDSFVTEQQ 10

RESULT 2
US-08-851-567B-2
; Sequence 2, Application US/08851567B
; Patent No. 6528484
; GENERAL INFORMATION:
; APPLICANT: Ensign, Jerald C
; APPLICANT: Bowen, David J
; APPLICANT: Petell, James
; APPLICANT: Fatig, Raymond
; APPLICANT: Schoonover, Sue
; APPLICANT: French-Constant, Richard
```

APPLICANT: Rochelleau, Thomas A.  
APPLICANT: Blackburn, Michael B.  
APPLICANT: Hey, Timothy D.  
APPLICANT: Merlo, Donald J.  
APPLICANT: Orr, Gregory L.  
APPLICANT: Roberts, Jean L.  
APPLICANT: Strickland, James A.  
APPLICANT: Guo, Lining  
APPLICANT: Ciche, Todd A.  
APPLICANT: Suknapiada, Kitiari  
TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Dow Agrosciences Patent Department  
STREET: 9330 Zionsville Road  
CITY: Indianapolis  
STATE: IN  
COUNTRY: US  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/851,567B  
FILING DATE: 05-MAY-1997  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/063,615  
FILING DATE: 18-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/395,497  
FILING DATE: 28-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/007,255  
FILING DATE: 06-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/608,423  
FILING DATE: 28-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/705,484  
FILING DATE: 28-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J  
REGISTRATION NUMBER: 27386  
REFERENCE/DOCKET NUMBER: 960296.93804  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: N-terminal  
US-08-851-567B-2

Query Match 33.5%; Score 28.5; DB 2; Length 12;  
Best Local Similarity 53.8%; Pred. No. 1.4e+02;  
Matches 7; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 3 DSPURTEQQAATW 15  
|||  
Db 3 DSP---EVSITW 12

RESULT 3  
US-09-339-922A-88  
Sequence 88, Application US/09339922A  
Patent No. 6531580

GENERAL INFORMATION:  
APPLICANT: Huse, William D.  
TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic  
FILE REFERENCE: P-IX 3536  
CURRENT APPLICATION NUMBER: US/09/339,922A  
CURRENT FILING DATE: 1999-06-24  
NUMBER OF SEQ ID NOS: 112  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 88  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Mutated  
OTHER INFORMATION: complementarity determining region (CDR)  
US-09-339-922A-88

Query Match 32.9%; Score 28; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 5e+05;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 QQAATW 15  
|||  
Db 1 QQSTW 6

RESULT 4  
US-09-016-061-88  
Sequence 88, Application US/09016061  
Patent No. 6596850  
GENERAL INFORMATION:  
APPLICANT: Huse, William D.  
APPLICANT: Glaser, Scott M.  
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human  
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use  
NUMBER OF SEQUENCES: 100  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Campbell & Flores LLP  
STREET: 4370 La Jolla Village Drive, Suite 700  
CITY: San Diego  
STATE: California  
COUNTRY: United States  
ZIP: 92122  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/016,061  
FILING DATE: 30-JAN-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/791,391  
FILING DATE: 30-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Campbell, Cathryn A.  
REGISTRATION/DOCKET NUMBER: 31,815  
REFERENCE/DOCKET NUMBER: P-IX 2965  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 535-9001  
TELEFAX: (619) 535-8949  
INFORMATION FOR SEQ ID NO: 88:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-016-061-88

Query Match 32.9%; Score 28; DB 2; Length 9;



Best Local Similarity 66.7%; Pred. No. 5e+05; Indels 0; Gaps 0;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 10 QOATW 15

Db 1 QOSTW 6

RESULT 5

5223254-6

; Patent No. 5223254

; APPLICANT: PARADISO, PETER R.; HILBRETH, STEPHEN W.; HU,

; BRANDA T.; MARTIN-GALLARDO, ANTONIA; ARUMUGHAM, RASAPPA

; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES

; NUMBER OF SEQUENCES: 17

; CURRENT APPLICATION DATA:

; FILING DATE: 20-SEP-1988

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 102,180

; FILING DATE: 29-SEP-1987

; SEQ ID NO: 6:

; LENGTH: 13

5223254-6

Query Match 32.9%; Score 28; DB 7; Length 13;  
Best Local Similarity 40.0%; Pred. No. 1.9e+02;

Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NDSPVTEQ 11

Db 2 NDMPITNDQK 11

RESULT 6

US-09-641-528B-48206

; Sequence 48206, Application US/09641528B

; Patent No. 7026443

; GENERAL INFORMATION:

; APPLICANT: Sette, Alessandro

; APPLICANT: Sidney, John

; APPLICANT: Southwood, Scott

; APPLICANT: Chesnut, Robert

; APPLICANT: Celis, Esleben

; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS

; FILE REFERENCE: 2060.0100001

; CURRENT APPLICATION NUMBER: US/09/641,528B

; PRIOR FILING DATE: 2000-08-15

; PRIOR APPLICATION NUMBER: US 60/172,705

; NUMBER OF SEQ ID NOS: 51505

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 48206

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Peptide Derived from Human Papillomavirus

US-09-641-528B-48206

Query Match 32.9%; Score 28; DB 3; Length 15;  
Best Local Similarity 42.9%; Pred. No. 2.2e+02;

Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQAT 14

Db 2 YNVSFVETVNEYNT 15

RESULT 7

US-08-836-075A-166

; Sequence 166, Application US/08836075A

; Patent No. 6180768

; GENERAL INFORMATION:

; APPLICANT: MAERTENS, GEERT

; APPLICANT: STUYVER, LIEVEN

; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES

; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC

; NUMBER OF SEQUENCES: 207

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ARNOLD, WHITE & DURKEE

; STREET: P.O. BOX 4433

; CITY: HOUSTON

; STATE: TEXAS

; COUNTRY: USA

; ZIP: 77210-4433

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Microsoft Word 6.0 / ASCII text output

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/836,075A

; FILING DATE: 21 Apr 1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/EP95/04155

; FILING DATE: 23 Oct 1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 94870166.9

; FILING DATE: 21 Oct 1994

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95870076.7

; FILING DATE: 28 Jun 1995

; ATTORNEY/AGENT INFORMATION:

; NAME: KAMMERER, PATRICIA A.

; REGISTRATION NUMBER: 29,775

; INFORMATION/DOCKET NUMBER: INNS:004

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-836-075A-166

Query Match 31.8%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 VRTGQATW 15

Db 1 VRTGQATW 10

RESULT 8

US-09-878-281A-244

; Sequence 244, Application US/09878281A

; Patent No. 6762024

; GENERAL INFORMATION:

; APPLICANT: Innogenetics N.V.

; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph.

; FILE REFERENCE: 35

; CURRENT APPLICATION NUMBER: US/09/878,281A

; CURRENT FILING DATE: 2001-06-12

; NUMBER OF SEQ ID NOS: 284

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 244

; LENGTH: 13

; TYPE: PRT

; ORGANISM: hepatitis C virus

US-09-878-281A-244

Query Match 31.8%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 VRTGQATW 15  
| | | | |  
Db 1 VRTGQGRCW 10

RESULT 9  
US-09-851-138C-166  
; Sequence 166, Application US/09851138C  
; Patent No. 6974864  
; GENERAL INFORMATION:  
; APPLICANT: INNOGENETICS N.V.  
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as  
; FILE REFERENCE: 2551-106  
; CURRENT APPLICATION NUMBER: US/09/851,138C  
; PRIOR FILING DATE: 2001-05-09  
; PRIOR APPLICATION NUMBER: EP 94870166.9  
; PRIOR FILING DATE: 1994-10-21  
; PRIOR APPLICATION NUMBER: EP 95870076.7  
; PRIOR FILING DATE: 1995-06-28  
; NUMBER OF SEQ ID NOS: 302  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 166  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: hepatitis C virus  
US-09-851-138C-166

Query Match 31.8%; Score 27; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 2.9e+02;  
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 VRTGQATW 15  
| | | | |  
Db 1 VRTGQGRCW 10

RESULT 10  
US-10-000-986A-144  
; Sequence 144, Application US/10000986A  
; Patent No. 7005500  
; GENERAL INFORMATION:  
; APPLICANT: Benjamin, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF  
; FILE REFERENCE: G-091US09DIIV  
; CURRENT APPLICATION NUMBER: US/10/000,986A  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: US 09/924,340  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/01715  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/305,456  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/302,277  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/298,698  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: US 60/293,574  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 228  
; SOFTWARE: JPatent  
; SEQ ID NO 144  
; LENGTH: 14  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-000-986A-144

Query Match 31.8%; Score 27; DB 3; Length 14;

Best Local Similarity 33.3%; Pred. No. 3.1e+02;  
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 HNSDPVTEQQA 12  
| | | | |  
Db 2 HSDSGISVDSQS 13

RESULT 11  
US-08-221-583-56  
; Sequence 56, Application US/08221583  
; Patent No. 5486595  
; GENERAL INFORMATION:  
; APPLICANT: Heaven, George A.  
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors  
; NUMBER OF SEQUENCES: 62  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595r1e  
; STREET: One Liberty Place 46th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: USA  
; ZIP: 19403  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctchod.  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,583  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Deluca, Mark  
; REGISTRATION NUMBER: 33,229  
; REFERENCE/DOCKET NUMBER: CCOR-0185  
; TELEPHONE: (215) 568-3439  
; TELEFAX: (215) 568-3439  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 15 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-221-583-56

Query Match 31.8%; Score 27; DB 1; Length 15;  
Best Local Similarity 46.2%; Pred. No. 3.4e+02;  
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 HNSDPVTEQQA 13  
| | | | |  
Db 1 HLPQVSTRSQHT 13

RESULT 12  
PCT-US95-04018-56  
; Sequence 56, Application PC/TUS9504018  
; GENERAL INFORMATION:  
; APPLICANT: Heaven, George A.  
; APPLICANT: Kruszynski, Marlen  
; APPLICANT: Mervic, Miljenko  
; APPLICANT: Weber, Robert W.  
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors  
; NUMBER OF SEQUENCES: 76  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &  
; STREET: One Liberty Place 46th Floor  
; CITY: Philadelphia  
; STATE: Pennsylvania  
; COUNTRY: USA

ZIP: 19403  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WordPerfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04018  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/221,580  
FILING DATE: 01-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/221,583  
FILING DATE: 01-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/221,581  
FILING DATE: 01-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Deluca, Mark  
REGISTRATION NUMBER: 33,229  
REFERENCE/DOCKET NUMBER: CCOR-0232  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-3100  
TELEFAX: (215) 568-3439  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PCT-US95-04018-56

Query Match 31.8%; Score 27; DB 5; Length 15;  
Best Local Similarity 46.2%; Pred. No. 3.4e+02;  
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQT 13  
Db 1 HLPQVSTRSQHT 13

RESULT 13  
US-09-641-528B-4922  
Sequence 4922, Application US/09641528B  
Patent No. 7026443  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Cells, Esteban  
APPLICANT: Grey, Howard  
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS  
FILE REFERENCE: 2060.0100001  
CURRENT APPLICATION NUMBER: US/09/641,528B  
CURRENT FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: US 60/172,705  
PRIOR FILING DATE: 1999-12-10  
NUMBER OF SEQ ID NOS: 51505  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 4922  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528B-4922

Query Match 30.6%; Score 26; DB 3; Length 9;  
Best Local Similarity 55.6%; Pred. No. 5e+05;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
Qy 6 VRIEQATT 14  
Db 1 VOVEEQOTT 9

RESULT 14  
US-09-641-528B-13784  
Sequence 13784, Application US/09641528B  
Patent No. 7026443  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Cells, Esteban  
APPLICANT: Grey, Howard  
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS  
FILE REFERENCE: 2060.0100001  
CURRENT APPLICATION NUMBER: US/09/641,528B  
CURRENT FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: US 60/172,705  
PRIOR FILING DATE: 1999-12-10  
NUMBER OF SEQ ID NOS: 51505  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13784  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528B-13784

Query Match 30.6%; Score 26; DB 3; Length 9;  
Best Local Similarity 57.1%; Pred. No. 5e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 9 EQQATTW 15  
Db 3 EQVSTW 9

RESULT 15  
US-09-641-528B-26852  
Sequence 26852, Application US/09641528B  
Patent No. 7026443  
GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Cells, Esteban  
APPLICANT: Grey, Howard  
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS  
FILE REFERENCE: 2060.0100001  
CURRENT APPLICATION NUMBER: US/09/641,528B  
CURRENT FILING DATE: 2000-08-15  
PRIOR APPLICATION NUMBER: US 60/172,705  
PRIOR FILING DATE: 1999-12-10  
NUMBER OF SEQ ID NOS: 51505  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 26852  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528B-26852

Query Match 30.6%; Score 26; DB 3; Length 9;

Best Local Similarity 57.1%; Pred. No. 5e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 EQARTW 15  
| : |  
Db 1 EQVSTW 7

Search completed: May 30, 2006, 11:11:06  
Job time : 23.333 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2006, 09:58:55 ; Search time 11.6667 Seconds  
(without alignments)  
123.707 Million cell updates/sec

Title: US-10-758-165A-2

Perfect score: 85

Sequence: 1 HNDSPVTEQQAATW 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	27.1	11	2	S71304
2	22	25.9	15	2	PA0062
3	21	24.7	12	2	I41235
4	21	24.7	13	2	PH0138
5	20	23.5	11	2	I52980
6	20	23.5	11	2	S39012
7	20	23.5	15	2	B60763
8	19	22.4	9	2	A61357
9	19	22.4	10	2	A61337
10	19	22.4	11	2	A29806
11	19	22.4	11	2	A49037
12	19	22.4	12	2	E58502
13	19	22.4	13	2	A60458
14	19	22.4	13	2	S36887
15	19	22.4	14	2	S74128
16	19	22.4	14	2	PM0147
17	19	22.4	15	2	JN0263
18	19	22.4	15	2	A36527
19	18	21.2	6	2	S78764
20	18	21.2	11	2	JQ2317
21	18	21.2	12	2	PD0021
22	18	21.2	12	2	C30503
23	18	21.2	13	2	S33273
24	18	21.2	13	2	S47376
25	18	21.2	14	2	PH1625
26	18	21.2	14	2	PH1627
27	18	21.2	15	2	P00195
28	18	21.2	15	2	S32677
29	18	21.2	15	2	PA0020

30	18	21.2	15	2	PA0058	protein QF200022 -
31	18	21.2	15	2	A49177	22K protein pI, mi
32	18	21.2	15	2	A53594	calnexin - mouse (
33	17	20.0	5	2	PT0580	T-cell receptor be
34	17	20.0	6	2	A31263	dihydrofolate redu
35	17	20.0	7	2	S33246	neuromodulatory pe
36	17	20.0	8	2	PT0030	inulinase (EC 3.2.
37	17	20.0	8	2	I57018	gene Cfr protein
38	17	20.0	9	2	PT0247	ig heavy chain CRD
39	17	20.0	10	2	S66248	processing enzyme,
40	17	20.0	10	2	A60722	cryptic fibritial p
41	17	20.0	10	2	S39030	lysl-bradykinin -
42	17	20.0	11	2	H54346	pyruvate synthase
43	17	20.0	11	2	B49037	TCR gamma V-J regi
44	17	20.0	11	2	C49037	TCR gamma V-J regi
45	17	20.0	11	2	A61512	variant surface gl

## ALIGNMENTS

```
RESULT 1
S71304
amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragment)
C:Species: Aspergillus niger
C>Date: 12-Feb-1998 #sequence_revision 01-May-1998 #text_change 09-Jul-2004
C/Accession: S71304
R:Frederic, I.; Tamaki, H.; Ishida, H.; Pec, P.; Luhova, L.; Tsuno, H.; Hata, M.; Asano
Eur. J. Biochem. 237, 255-265, 1996
A:Title: Two distinct quinoprotein amine oxidases are induced by n-butylamine in the myc
A:Reference number: S71303; MUID:96203933; PMID:8620882
A:Accession: S71304
A:Molecule type: protein
A:Residues: 1-11 <FRE>
A:Cross-references: UNIPROT:Q7M504; UNIPARC:UPI000017B3B7
C:Keywords: copper binding; monomer; oxidoreductase; quinoprotein; topaquione

Query Match          27.1%  Score 23;  DB 2;  Length 11;
Best Local Similarity 100.0%;  Pred. No. 6.7e+02;
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

OY      2 NDSP 5
DB      1 NDSP 4

RESULT 2
PA0062
fumarate hydratase (EC 4.2.1.2) - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: PA0062
R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPD, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0051
A:Accession: PA0062
A:Molecule type: protein
A:Residues: 1-15 <CHO>
A:Cross-references: UNIPROT:Q7M423; UNIPARC:UPI000017B3FD
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match          25.9%  Score 22;  DB 2;  Length 15;
Best Local Similarity 55.6%;  Pred. No. 1.4e+03;
Matches 5;  Conservative 0;  Mismatches 4;  Indels 0;  Gaps 0;

OY      4 SPVTEQQA 12
DB      1 SQRTESDA 9

RESULT 3
I41235
```

glutamine-tRNA ligase (EC 6.1.1.18) - *Escherichia coli* (fragment)  
 C/Species: *Escherichia coli*  
 C/Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 03-Jun-2002  
 C/Accession: 141235  
 R/Hoben, P.; Uemura, H.; Yamao, F.; Cheung, A.; Swanson, R.; Sumner-Smith, M.; Soli, D.  
 Fed. Proc. 43, 2972-2976, 1984  
 A/Title: Misamincacylation by glutamyl-tRNA synthetase: relaxed specificity in wild-type  
 A/Reference number: 141235; MUID:85051900; PMID:6389180  
 A/Accession: 141235  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-12 <RES>  
 A/Cross-references: UNIPARC:UPI000016F1B4; GB:M16470; NID:G146170; PIDN:AAA69006.1; PID:  
 C/Keywords: aminocyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 24.7%; Score 21; DB 2; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 1.7e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 11 QATTW 15  
 Db 3 EAETW 7

RESULT 4  
 PH0138  
 T-cell receptor beta chain V-D-J region C8 - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 30-May-1997  
 C/Accession: PH0138  
 R/Martin, R.; Howell, M.D.; Jaraquemada, D.; Flerlage, M.; Richey, J.; Brostoff, S.; Le  
 J. Exp. Med. 173, 19-24, 1991  
 A/Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the context  
 A/Reference number: PH0135; MUID:91086843; PMID:1702137  
 A/Accession: PH0138  
 A/Molecule type: mRNA  
 A/Residues: 1-13 <MAR>  
 A/Cross-references: UNIPARC:UPI000017C3AC  
 C/Keywords: T-cell receptor

Query Match 24.7%; Score 21; DB 2; Length 13;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+03;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 12 ATTW 15  
 Db 4 ASTM 7

RESULT 5  
 152980  
 glucocerebrosidase - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
 C/Accession: 152980; 165971  
 R/Reiner, O.; Wiggerson, M.; Horowitz, M.  
 DNA 7, 107-116, 1988  
 A/Title: Structural analysis of the human glucocerebrosidase genes.  
 A/Reference number: 152980; MUID:88195776; PMID:3358914  
 A/Accession: 152980  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-11 <RES>  
 A/Cross-references: UNIPARC:UPI000016A981; GB:M18916; NID:G183023; PIDN:AAA35878.1; PID:  
 A/Accession: 165971  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-11 <RES>  
 A/Cross-references: UNIPARC:UPI000016A981; GB:M18917; NID:G183025; PIDN:AAA35879.1; PID:  
 Query Match 23.5%; Score 20; DB 2; Length 11;  
 Best Local Similarity 100.0%; Pred. No. 2.3e+03;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 SPVR 7  
 Db 5 SPVR 8

RESULT 6  
 S39012  
 proteinase - *Thermus* sp.  
 C/Species: *Thermus* sp.  
 C/Date: 18-Feb-1994 #sequence\_revision 19-Apr-1996 #text\_change 07-May-1999  
 C/Accession: S39012  
 R/Fireman, S.A.; Peek, K.; Prescott, M.; Daniel, R.  
 Biochem. J. 295, 463-469, 1993  
 A/Title: Characterization of a chelator-resistant proteinase from *Thermus* strain Rt4A2.  
 A/Reference number: S39012; MUID:94058984; PMID:8240244  
 A/Accession: S39012  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-15 <FRE>  
 A/Cross-references: UNIPARC:UPI00000BBFF9  
 A/Note: 13-Ala was also found

Query Match 23.5%; Score 20; DB 2; Length 15;  
 Best Local Similarity 50.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 10 QOATTW 15  
 Db 3 OSPVTW 8

RESULT 7  
 B60763  
 endo-1,3-beta-glucanase (EC 3.2.1.-), 40k - *Bacillus circulans* (strain W1-12) (fragment)  
 C/Species: *Bacillus circulans*  
 C/Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 09-Jul-2004  
 C/Accession: B60763  
 R/Fiske, M.J.; Tobey-Fincher, K.L.; Fuchs, R.L.  
 J. Gen. Microbiol. 136, 2377-2383, 1990  
 A/Title: Cloning of two genes from *Bacillus circulans* W1-12 which encode 1,3-beta-glucan  
 A/Reference number: A60763; MUID:91178514; PMID:2127800  
 A/Accession: B60763  
 A/Molecule type: protein  
 A/Residues: 1-15 <FIS>  
 A/Cross-references: UNIPROT:Q7ML10; UNIPARC:UPI000017AC94  
 C/Comment: This bacillus produces up to six different 1,3-beta-glucanases for growth on c  
 C/Keywords: glycosidase; hydrolase

Query Match 23.5%; Score 20; DB 2; Length 15;  
 Best Local Similarity 75.0%; Pred. No. 3.2e+03;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 12 ATTW 15  
 Db 1 ATWW 4

RESULT 8  
 A61357  
 phytocearulein - *Sauvage's* leaf frog  
 C/Species: *Phyllomedusa sauvagei* (*Sauvage's* leaf frog)  
 C/Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 09-Jul-2004  
 C/Accession: A61357  
 R/Ansaldi, A.; Bertaccini, G.; Cai, J.M.; De Caro, G.; Erspamer, V.; Impicciatore, M.  
 Br. J. Pharmacol. 37, 198-206, 1969  
 A/Title: Structure and pharmacological actions of phytocearulein, a caerulein-like nonaf  
 A/Reference number: A61357; MUID:70005484; PMID:5824931  
 A/Accession: A61357  
 A/Status: preliminary  
 A/Molecule type: protein  
 A/Residues: 1-9 <ANA>  
 A/Cross-references: UNIPROT:Q7LZC4; UNIPARC:UPI000017668D

C:Superfamily: gastrin  
 C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; skin; sulfoprotein  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:3/Binding site: sulfate (Tyr) (covalent) #status experimental  
 F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 22.4%; Score 19; DB 2; Length 9;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 QOATW 15  
 Db 1 QEYTCW 6

RESULT 9  
 A61337  
 caerulein - frog (Hyla caerulea)  
 C:Species: Hyla caerulea  
 C>Date: 05-Aug-1994 #sequence\_revision 05-Aug-1994 #text\_change 07-May-1999  
 C:Accession: A61337  
 R:Anastasi, A.; Expmeyer, V.; Endean, R.  
 Arch. Biochem. Biophys. 125, 57-68, 1968  
 A:Title: Isolation and amino acid sequence of caerulein, the active decapeptide of the S  
 A:Reference number: A61337; MUID:68238534; PMID:5649531  
 A:Accession: A61337  
 A:Molecule type: protein  
 A:Residues: 1-10 <ANA>  
 A:Cross-references: UNIPARC:UPI0000126DC  
 C:Comment: The last five amino acids and the carboxyl terminal amide group of this neuro  
 C:Superfamily: gastrin  
 C:Keywords: amidated carboxyl end; antihypertensive; neuropeptide; pyroglutamic acid; se  
 F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
 F:4/Binding site: sulfate (Tyr) (covalent) #status experimental  
 F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 22.4%; Score 19; DB 2; Length 10;  
 Best Local Similarity 42.9%; Pred. No. 3.1e+03;  
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 EQOATW 15  
 Db 1 QOQDTGW 7

RESULT 10  
 A29806  
 acidic proline-rich protein HP43b - golden hamster (fragment)  
 C:Species: Mesocricetus auratus (golden hamster)  
 C>Date: 19-May-1989 #sequence\_revision 19-May-1989 #text\_change 18-Jun-1993  
 C:Accession: A29806  
 R:Mahanhho, H.; Ann, D.K.; Butler, L.G.; Rogler, J.; Carlson, D.M.  
 J. Biol. Chem. 262, 12344-12350, 1987  
 A:Title: Induction of proline-rich proteins in hamster salivary glands by isoproterenol  
 A:Reference number: A92611; MUID:87308247; PMID:3040740  
 A:Accession: A29806  
 A:Molecule type: protein  
 A:Residues: 1-11 <MEH>  
 A:Cross-references: UNIPARC:UPI000017C60F

Query Match 22.4%; Score 19; DB 2; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 3.4e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HNDSP 5  
 Db 4 YEDSP 8

RESULT 11  
 A49037  
 TCR gamma V-J region - mouse (fragment)

C:Species: Mus musculus (house mouse)  
 C>Date: 21-Jan-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
 C:Accession: A49037  
 R:Ezqueria, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.M.  
 Eur. J. Immunol. 22, 491-498, 1992  
 A:Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T  
 A:Reference number: A49037; MUID:92164730; PMID:1311262  
 A:Accession: A49037  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-11 <EQZ>  
 A:Cross-references: UNIPARC:UPI00001154FA; GB:S90637; NID:G246288; PIDN:AB21547.1; PID:9  
 A:Experimental source: dendritic epidermal T-cell lines  
 A>Note: sequence extracted from NCBI backbone (NCBIN:90637, NCBI:90641)

Query Match 22.4%; Score 19; DB 2; Length 11;  
 Best Local Similarity 40.0%; Pred. No. 3.4e+03;  
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 11 QATW 15  
 Db 6 RSTW 10

RESULT 12  
 E58502  
 43.2K bile stone protein - unidentified bacterium (fragment)  
 C:Species: unidentified bacterium  
 C>Date: 07-Feb-1997 #sequence\_revision 07-Feb-1997 #text\_change 09-Jul-2004  
 C:Accession: E58502  
 R:Binette, J.P.; Binette, M.B.  
 submitted to the Protein Sequence Database, October 1996  
 A:Description: The proteins of kidney and gallbladder stones.  
 A:Reference number: A58501  
 A:Accession: E58502  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-12 <BIN>  
 A:Cross-references: UNIPROT:Q7M1D0; UNIPARC:UPI000017ABD4  
 A:Experimental source: human bile with stones  
 A>Note: a secondary sequence DVKIGVAGS was also found

Query Match 22.4%; Score 19; DB 2; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 3.8e+03;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NDSPV 6  
 Db 6 NEQPV 10

RESULT 13  
 A60458  
 protocatechuate 3,4-dioxygenase (EC 1.13.11.3) alpha chain - Moraxella sp. (strain GU2)  
 N:Alternate names: protocatechuate oxygenase  
 C:Species: Moraxella sp.  
 C>Date: 20-Feb-1993 #sequence\_revision 20-Feb-1993 #text\_change 07-May-1999  
 C:Accession: A60458  
 R:Sterliades, R.; Pelmont, J.  
 Appl. Environ. Microbiol. 55, 340-347, 1989  
 A:Title: Occurrence of two different forms of protocatechuate 3,4-dioxygenase in a Morax  
 A:Reference number: A60458; MUID:89245845; PMID:2541659  
 A:Accession: A60458  
 A:Molecule type: protein  
 A:Residues: 1-13 <STE>  
 A:Cross-references: UNIPARC:UPI000017A9FE  
 A>Note: two forms P and G of the alpha subunit yielded identical amino terminal sequences  
 C:Keywords: iron; oxidoreductase

Query Match 22.4%; Score 19; DB 2; Length 13;  
 Best Local Similarity 44.4%; Pred. No. 4.1e+03;  
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 7 RTEOATW 15  
 ||:|:|:  
 Db 3 RTAKPPTY 11

## RESULT 14

S36887  
 ribosomal protein S14 - Mycobacterium bovis (fragments)  
 C:Species: Mycobacterium bovis  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 13-Jan-1995  
 C:Accession: S36887  
 R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.  
 FEBS Lett. 331, 9-14, 1993  
 A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobac  
 A:Reference number: S36887; MUID:94009553; PMID:8405418  
 A:Accession: S36887  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-2;3-12;13 <OH>  
 A:Cross-references: UNIPARC:UPI000061DAD; UNIPARC:UPI000011EC65; UNIPARC:UPI000017AD47  
 C:Keywords: protein biosynthesis; ribosome

Query Match 22.4%; Score 19; DB 2; Length 13;  
 Best Local Similarity 37.5%; Pred. No. 4.1e+03;  
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 6 VRTEOQAT 13  
 |:.:|||  
 Db 6 VKNGRRAT 13

## RESULT 15

S74128  
 superoxide dismutase (EC 1.15.1.1) 1 (Ni) - Streptomyces coelicolor (fragment)  
 C:Species: Streptomyces coelicolor  
 C>Date: 11-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 07-May-1999  
 C:Accession: S74128  
 R:Kim, E.J.; Kim, H.P.; Hah, Y.C.; Roe, J.H.  
 Eur. J. Biochem. 241, 178-185, 1996  
 A:Title: Differential expression of superoxide dismutases containing Ni and Fe/Zn in Str  
 A:Reference number: S74128; MUID:97054607; PMID:8898904  
 A:Accession: S74128  
 A:Molecule type: protein  
 A:Residues: 1-14 <KIM>  
 A:Cross-references: UNIPARC:UPI000017AE10  
 A:Experimental source: ATCC 10147  
 C:Function:  
 A:Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen  
 C:Keywords: metalloprotein; nickel; oxidoreductase; tetramer

Query Match 22.4%; Score 19; DB 2; Length 14;  
 Best Local Similarity 60.0%; Pred. No. 4.5e+03;  
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HNDSP 5  
 |||  
 Db 1 HGDLF 5

Search completed: May 30, 2006, 10:13:20  
 Job time : 13 secs





OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OK NCBI\_TaxID=10090;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Balb/c; TISSUE=Liver;  
RX MEDLINE=94250690; PubMed=8193161;  
RA Baumgartner B., Heiland S., Kunze N., Richter A., Knippers R.;  
RT "Conserved regulatory elements in the type I DNA topoisomerase gene  
promoters of mouse and man.";  
RL Biochim. Biophys. Acta 1218:123-127(1994).  
RN (2)  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=Balb/c; TISSUE=Liver;  
RA Baumgartner B.;  
RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.  
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CC -----  
DR EMBL; X70958; CA50294.1; -; Genomic\_DNA.  
DR MGI; MGI:98788; Top1.  
DR GO; GO:0006260; P:DNA replication; IMP.  
KW Isomerase.  
FT NON TER 11 11  
SQ SEQUENCE 11 AA; 1240 MW; 95183A9D41E721EA CRC64;

Query Match 28.2%; Score 24; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 4.6e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 HNDS 4  
Db 7 HNDS 10

RESULT 3  
ID Q7M504 ASPNG PRELIMINARY; PRT; 11 AA.  
AC Q7M504;  
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.  
DT 15-DEC-2003, sequence version 1.  
DT 07-FEB-2006, entry version 8.  
DE Amine oxidase (copper-containing) (EC 1.4.3.6) II (Fragment).  
OS Aspergillus niger.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
OK NCBI\_TaxID=5061;  
RN (1)  
RP PROTEIN SEQUENCE.  
RX MEDLINE=96203933; PubMed=8620882;  
RA Fredort J., Tamaki H., Ishida H., Pec P., Luhova L., Tsuno H.,  
RA Hatata M., Asano Y., Kato Y., Matsushita K., Toyama H., Kumagai H.,  
RA Adachi O.;  
RT "Two distinct quinoxaline amine oxidases are induced by n-butyamine  
in the mycelia of Aspergillus niger AKU 3302. Purification,  
characterization, cDNA cloning and sequencing.";  
RL Eur. J. Biochem. 237:255-265(1996).  
RN (2)  
RP NUCLEOTIDE SEQUENCE.  
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CC -----  
DR PIR; S71304; S71304.  
DR GO; GO:0008131; F:amine oxidase activity; IEA.  
FT NON TER 1 1  
SQ SEQUENCE 11 AA; 1158 MW; 21BBFPCA4472DC7 CRC64;

Query Match 27.1%; Score 23; DB 2; Length 11;  
Best Local Similarity 100.0%; Pred. No. 6.9e+03;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NDSP 5  
Db 1 NDSP 4

RESULT 4  
ID Q47602 ECOLI PRELIMINARY; PRT; 11 AA.  
AC Q47602;  
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
DT 01-NOV-1996, sequence version 1.  
DT 07-FEB-2006, entry version 16.  
DE Rase protein (Fragment).  
GN Name=Rase;  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OK NCBI\_TaxID=562;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=91139577; PubMed=1995588;  
RA Tao T., Bourne J.C., Blumenthal R.M.;  
RT "A family of regulatory genes associated with type II restriction-  
modification systems.";  
RL J. Bacteriol. 173:1367-1375(1991).  
RN (2)  
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CC -----  
DR EMBL; M63620; AAA24558.1; -; Genomic\_DNA.  
FT NON TER 11 11  
SQ SEQUENCE 11 AA; 1412 MW; 80ABB190C736DAAA CRC64;

Query Match 25.9%; Score 22; DB 2; Length 11;  
Best Local Similarity 44.4%; Pred. No. 1e+04;  
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
Qy 7 RTEQATW 15  
Db 3 RDDQLFTW 11

RESULT 5  
ID Q50117 MYCLE PRELIMINARY; PRT; 13 AA.  
AC Q50117;  
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
DT 01-NOV-1996, sequence version 1.  
DT 07-FEB-2006, entry version 17.  
DE U650W.  
OS Mycobacterium leprae.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OK NCBI\_TaxID=1769;  
RN (1)  
RP NUCLEOTIDE SEQUENCE.  
RA Smith D.R.;  
RT Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.  
RN (2)  
RP NUCLEOTIDE SEQUENCE.  
RA Robinson K.;  
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.  
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CC -----  
DR EMBL; U15184; AAA63055.1; -; Genomic\_DNA.  
SQ SEQUENCE 13 AA; 1503 MW; CAABF1429DEDS412 CRC64;

Query Match 25.9%; Score 22; DB 2; Length 13;  
Best Local Similarity 80.0%; Pred. No. 1.2e+04;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 DSPVR 7  
Db 3 DEPV 7

## RESULT 6

O7M423\_FUSSP PRELIMINARY; PRT: 15 AA.  
AC O7M423\_15-DEC-2003, integrated into UniProtKB/TrEMBL.  
DT 15-DEC-2003, sequence version 1.  
DE 07-FEB-2006, entry version 6.  
OS Fumarate hydratase (EC 4.2.1.2) (Fragment).  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.  
OX NCBI\_TaxID=5514;  
RN [1]  
RP PROTEIN SEQUENCE.  
RA Chow L.P., Fukaya N., Sugitara Y., Ueno Y., Tabuchi K., Taugita A.;  
RL Submitted (OCT-1994) to the PIR data bank.  
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-----  
DR PIR; PA0062; PA0062.  
DR GO; GO:0004333; F: fumarate hydratase activity; IEA.  
FT NON TER 1  
SQ SEQUENCE 15 AA; 1668 MW; 805C8118C239DE05 CRC64;

Query Match 25.9%; Score 22; DB 2; Length 15;  
Best Local Similarity 55.6%; Pred. No. 1.4e+04;  
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
OY 4 SPVTEQOA 12  
Db 1 SQRTESDA 9

## RESULT 7

O9TS39\_9PRIM PRELIMINARY; PRT: 15 AA.  
AC O9TS39\_01-MAY-2000, integrated into UniProtKB/TrEMBL.  
DT 01-MAY-2000, sequence version 1.  
DE 07-FEB-2006, entry version 7.  
OS Dopamine D5 (Fragment).  
OC Gorilla gorilla (Gorilla).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
OC Gorilla.  
OX NCBI\_TaxID=9593;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=92068184; PubMed=1958184;  
RA Nguyen T., Sunahara R., Marchese A., Van Tol H.H., Seeman P.,  
RA O'Dowd B.F.;  
RT "Transcription of a human dopamine D5 pseudogene";  
RL Biochem. Biophys. Res. Commun. 181:16-21(1991).  
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-----  
FT NON TER 1  
SQ SEQUENCE 15 AA; 1637 MW; 39D8326BA63BB90B CRC64;

Query Match 25.3%; Score 21.5; DB 2; Length 15;  
Best Local Similarity 33.3%; Pred. No. 1.8e+04;  
Matches 5; Conservative 1; Mismatches 2; Indels 7; Gaps 1;  
OY 1 HNDSPVTEQOATW 15

Db 1 HRD-----QASW 8

## RESULT 8

CWP06\_PHAVU STANDARD; PRT: 9 AA.  
ID CWP06\_PHAVU  
AC P80765;  
DT 27-SEP-2005, integrated into UniProtKB/Swiss-Prot.  
DT 27-SEP-2005, sequence version 1.  
DE 07-MAR-2006, entry version 5.  
DE 60 kDa cell wall protein (Fragment).  
OS Phaseolus vulgaris (Kidney bean) (French bean).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
OC Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
OC Phaseolus.  
OX NCBI\_TaxID=3885;  
RN [1]  
RP PROTEIN SEQUENCE. AND SUBCELLULAR LOCATION.  
RX MEDLINE=97332671; PubMed=9188482; DOI=10.1074/jbc.272.25.15841;  
RA Robertson D., Mitchell G.P., Gilroy J.S., Gerrish C., Bolwell G.P.,  
RA Slabas A.R.;  
RT "Differential extraction and protein sequencing reveals major  
RT differences in patterns of primary cell wall proteins from plants";  
RL J. Biol. Chem. 272:15841-15848(1997).  
CC -1- SUBCELLULAR LOCATION: Secreted; cell wall.  
CC  
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-----  
KW Cell wall; Direct protein sequencing.  
FT CHAIN 1  
FT NON TER 9  
SQ SEQUENCE 9 AA; 1160 MW; 9270B1A9C32B5DDA CRC64;

Query Match 24.7%; Score 21; DB 1; Length 9;  
Best Local Similarity 100.0%; Pred. No. 2.8e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 13 TTV 15  
Db 7 TTV 9

## RESULT 9

O798K5\_STRLI PRELIMINARY; PRT: 9 AA.  
ID O798K5\_STRLI  
AC O798K5\_05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DE 07-FEB-2006, entry version 6.  
DE AmlB protein (Fragment).  
CN Name=amlB;  
OS Streptomyces lividans.  
OC Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1916;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=98332731; PubMed=9666116; DOI=10.1016/S0378-1119(98)00265-0;  
RA Yin X.H., Gerbaud C., Franou F.A., Guerin M., Virolle M.J.;  
RT "amlC, another amyloid gene maps close to the amlB locus in  
RT Streptomyces lividans TK24";  
RL Gene 215:171-180(1998).  
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-----  
DR EMBL; Z86113; CAB06815.1; -; genomic\_DNA.  
FT NON TER 9  
SQ SEQUENCE 9 AA; 970 MW; F334C775A1A44871 CRC64;

```

Query Match          24.7%; Score 21; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDSPVR 7
   |||
Db 4 NTSPAR 9

RESULT 10
O9R635 CHLTR PRELIMINARY; PRT; 9 AA.
ID O9R635 CHLTR PRELIMINARY; PRT; 9 AA.
AC O9R635
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Major outer membrane protein variable domain IV, MOMP VD IV
DE (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydia.
OC NCBI_TaxID=813;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92040090; PubMed=1718870;
RA Peterson E.M., Cheng X., Markoff B.A., Fielder T.J., de la Maza L.M.,
RT "Functional and structural mapping of Chlamydia trachomatis species-
RT specific major outer membrane protein epitopes by use of neutralizing
RT monoclonal antibodies."
RL Infect. Immun. 59:4147-4153(1991).
CC -----
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CC -----
DR PIR; S16034; S16034.
FT NON_TER 1
FT NON_TER 9
SQ SEQUENCE 9 AA; 976 MW; 9C61B041B7645361 CRC64;

Query Match          24.7%; Score 21; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 TTV 15
   |||
Db 1 TTV 3

RESULT 11
O4A3D9 OENOE PRELIMINARY; PRT; 10 AA.
ID O4A3D9 OENOE PRELIMINARY; PRT; 10 AA.
AC O4A3D9
DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 13-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 2.
DE Cipl2 protein (Fragment).
DE Name=cipl2;
OS Oenococcus oeni (Leuconostoc oenos).
OC Bacteria; Firmicutes; Lactobacillales; Oenococcus.
OC NCBI_TaxID=1247;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=IOB 8413;
RA Grandvalet C., Couchehey F., Beltramo C., Guzzo J.;
RT "CsrR is the Master Regulator of Stress Response Gene Expression
RT in Oenococcus oeni."
RL J. Bacteriol. 147:5614-5623(2005).
CC -----
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CC -----
DR EMBL; AJ990337; CA165389.1; -; Genomic_DNA.
FT NON_TER 10
FT NON_TER 10

```

```

SQ SEQUENCE 10 AA; 1186 MW; 9693EE6AAA45B5A CRC64;

Query Match          24.7%; Score 21; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.4e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HNDSP 5
   |||
Db 4 YNDP 8

RESULT 12
O5EDJ3 LEGPN PRELIMINARY; PRT; 11 AA.
ID O5EDJ3 LEGPN PRELIMINARY; PRT; 11 AA.
AC O5EDJ3
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE Putative acyl carrier protein (Fragment).
DE Legionella pneumophila
OS Legionella pneumophila
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OC NCBI_TaxID=446;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=02/41;
RA Newton H.J., Hartland E.L.;
RT "Subtractive hybridization reveals DNA fragments present in Legionella
RT pneumophila, strain 02/41, and absent in Legionella micdadei, strain
RT 02/42."
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; AY902880; AAW83806.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 11 AA; 1159 MW; DCC78B8601ADC6C6 CRC64;

Query Match          24.7%; Score 21; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 9 EQOAT 13
   |||
Db 3 QOQAT 7

RESULT 13
EP65 HUMAN STANDARD; PRT; 13 AA.
ID EP65 HUMAN STANDARD; PRT; 13 AA.
AC P54963
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Erythrocyte 65 kDa protein (P65) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE.
RX MEDLINE=90004678; PubMed=2507249;
RA Hart G.W., Hattwanger R.S., Holt G.D., Kelly W.G.;
RT "Nucleoplasmic and cytoplasmic glycoproteins."
RL Ciba Found. Symp. 145:102-118(1989).
CC -----
CC -1- SUBCELLULAR LOCATION: Cytoplasm.
CC -----
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CC -----
DR GO; GO:0005737; C:cytoplasm; NAS.

```

```

KW Direct protein sequencing; Glycoprotein.
FT CHAIN <1 >13 Erythrocyte 65 kDa protein.
FT CARBOHYD 2 2 O-linked (GlcNAc).
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA: 1300 MW: D08B73344C61A776 CRC64;

Query Match 24.7%; Score 21; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DSPV 6
DB 1 DSPV 4

RESULT 14
Q9SB03 ORYSA PRELIMINARY; PRT; 13 AA.
AC Q9SB03;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE 07-FEB-2006, entry version 12.
DE Waxy (Fragment).
GN Name=Waxy;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98384837; PubMed=9718725;
RA Hirano H., Biguchi M., Sano Y.;
RT "A single base change altered the regulation of the Waxy gene at the
RT post-transcriptional level during domestication of rice.";
RL Mol. Biol. Evol. 15:978-987(1998).
CC -----
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CC -----
DR EMBL: AB008794; BAA32471.1; -; Genomic_DNA.
DR Gramene; Q9SB03; -.
DR GO; GO:0004373; F:glycogen (starch) synthase activity; IEP.
DR GO; GO:0005982; P:starch metabolism; IEP.
FT NON_TER 13
SQ SEQUENCE 13 AA: 1281 MW: 999F8DEB570FCSA1 CRC64;

Query Match 24.7%; Score 21; DB 2; Length 13;
Best Local Similarity 45.5%; Pred. No. 1.9e+04;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 SPVTEQATT 14
DB 2 SALTSQLATS 12

RESULT 15
Q7IGS6 GHYME PRELIMINARY; PRT; 14 AA.
AC Q7IGS6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 07-MAR-2006, entry version 8.
DE Cytochrome oxidase subunit I (Fragment).
OS Andrena n. sp. 'goth'.
OS Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apoidea; Aculeata; Apoidea;
OC Andrenidae; Andreninae; Andrena; Callandrena.
OX NCBI_TaxID=205171;
RN [1]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=96;
RX PubMed=16343953; DOI=10.1016/j.ympev.2005.10.003;
RA Larkin L.L., Neff J.L., Simpson B.B.;
RT "Phylogeny of the Callandrena subgenus of Andrena (Hymenoptera:
RT Andrenidae) based on mitochondrial and nuclear DNA data: Polyphyly and
RT convergent evolution.";
RL Mol. Phylogenet. Evol. 38:330-343 (2006).
CC -----
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CC -----
DR EMBL: AF504376; AA007723.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
FT NON_TER 1
SQ SEQUENCE 14 AA: 1692 MW: 79E3B922A4E7B5B CRC64;

Query Match 24.7%; Score 21; DB 2; Length 14;
Best Local Similarity 37.5%; Pred. No. 2e+04;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPVTE 9
DB 6 NEIPIMTK 13

Search completed: May 30, 2006, 11:09:59
Job time : 72.333 secs

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OM protein - protein search, using sw model

Run on: May 30, 2006, 09:58:50 ; Search time 60 Seconds  
(without alignments)  
114.304 Million cell updates/sec

Title: US-10-758-165A-2  
Perfect score: 85  
Sequence: 1 HNDSPVTEQQTW 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 837128

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003s:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*
- 9: Geneseqp2005s:\*
- 10: Geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	100.0	15	8	ADRI0602 Cat IGE e
2	48	56.5	15	8	ADRI0601 Dog IGE e
3	39	46.9	15	8	ADRI0607 Pig IGE e
4	37	43.5	15	8	ADRI0603 Horse IGE
5	35	41.2	15	7	ADCI4568 Horse Imm
6	32	37.6	10	5	AAU79709 Synthetic
7	30	35.3	10	3	AAI38098 Human ABC
8	29	34.1	15	4	AAI55476 Human e1a
9	29	34.1	15	2	AAI55733 dedNA-dep
10	29	34.1	15	8	ADP97089 Cysteine
11	28.5	33.5	12	2	AAI56548 Toxin fra
12	28	32.9	9	2	AAW76034 LM609 gra
13	28	32.9	9	4	AAI61392 Mutant VL
14	28	32.9	9	6	ABO19830 Enhanced
15	28	32.9	9	6	ABR62303 Surface s
16	28	32.9	9	7	ADG71862 Enhanced
17	28	32.9	9	8	ADJ58043 Murine LM
18	28	32.9	9	8	ADJ73181 CDR3 of t
19	28	32.9	10	5	ABG98755 F protein
20	28	32.9	13	7	AAI79898 Fusion pr
21	28	32.9	15	7	ADW62941 Human 98P
22	28	32.9	15	7	ADW63829 Human 98P
23	27	31.8	8	2	AAW59312 Non-polio

24	27	31.8	9	3	AAI10015	AAI10015 H. pylori
25	27	31.8	9	4	AAI86095	AAI86095 H. pylori
26	27	31.8	9	4	AAI86063	AAI86063 H. pylori
27	27	31.8	9	5	AAI99231	AAI99231 CD45RO/RB
28	27	31.8	9	5	AAU72845	AAU72845 Anti-NGG2
29	27	31.8	9	5	AAU72853	AAU72853 Anti-NGG2
30	27	31.8	9	9	ADY80269	ADY80269 CDR3 from
31	27	31.8	9	9	ADY80269	ADY80269 CDR3 from
32	27	31.8	9	9	ADY80269	ADY80269 CDR3 from
33	27	31.8	9	10	AAE21780	AAE21780 Humanized
34	27	31.8	10	5	ABG98754	ABG98754 F protein
35	27	31.8	13	2	AAI63411	AAI63411 Peptide f
36	27	31.8	13	2	AAI63411	AAI63411 Peptide f
37	27	31.8	14	4	AAI97114	AAI97114 Human pep
38	27	31.8	14	8	ADT40356	ADT40356 hSARS vir
39	27	31.8	14	8	ADT37886	ADT37886 hSARS vir
40	26	30.6	8	2	AAI04462	AAI04462 Active m1
41	26	30.6	9	6	ABP74676	ABP74676 Human SCP
42	26	30.6	9	6	AAE38100	AAE38100 Human COU
43	26	30.6	9	7	ADCO9535	ADCO9535 Epitope w
44	26	30.6	9	8	ADN28303	ADN28303 Human CD3
45	26	30.6	10	2	AAI04464	AAI04464 Active m1

## ALIGNMENTS

RESULT 1  
ID ADR10602 standard; peptide: 15 AA.  
XX  
AC ADR10602;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Cat IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.  
XX  
KW Antiaesthatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
KW cat.  
XX  
OS Fells catus.  
XX  
FN WO2004065936-A2.  
XX  
PD 05-AUG-2004.  
XX  
PF 15-JAN-2004; 2004WO-US003566.  
XX  
PR 16-JAN-2003; 2003US-0440472P.  
XX  
PA (UYNC-) UNIV NORTH CAROLINA STATE.  
XX  
PI Hammerberg B;  
XX  
DR WPI; 2004-593545/57.  
XX  
PT Novel antibody that specifically binds to mammalian IGE epitope, useful  
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
PT or treating asthma or anaphylactic shock.  
XX  
PS Example 6; Page 9; 14pp: English.  
XX  
CC The present invention relates to a novel monoclonal antibody (I) that  
CC specifically binds to a mammalian IGE epitope, where the epitope is  
CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
CC and corn allergens. The sample is a biological sample collected from a  
CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the





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ID  ADR10603 standard; peptide; 15 AA.
XX
XX  ADR10603;
XX
AC  21-OCT-2004 (first entry)
XX
DT  21-OCT-2004 (first entry)
XX
DE  Horse IGE epitope recognised by monoclonal antibody 5.91. SEQ ID 3.
XX
XX  Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
KM  anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
XX  horse.
XX  Equus caballus.
OS
XX  WO2004065936-A2.
XX
XX  05-AUG-2004.
XX
XX  15-JAN-2004; 2004WO-US003566.
XX
XX  16-JAN-2003; 2003US-0440472P.
XX
XX  (UNNC-) UNIV NORTH CAROLINA STATE.
XX
XX  Hammerberg B;
XX
XX  WPI; 2004-593545/57.
XX
XX  Novel antibody that specifically binds to mammalian IGE epitope, useful
PT  for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT  or treating asthma or anaphylactic shock.
XX
XX  Example 6; Page 9; 14pp; English.
XX
XX  The present invention relates to a novel monoclonal antibody (I) that
CC  specifically binds to a mammalian IGE epitope, where the epitope is
CC  between amino acids 146-166 or 356-374 of mammalian IGE, e.g. dog IGE.
XX  (I) is useful for testing an allergen reactivity of an IGE sample. The
CC  allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC  and corn allergens. The sample is a biological sample collected from a
CC  dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
CC  treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC  antibodies recognise epitopes on canine IGE corresponding to amino acid
CC  residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
CC  canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
CC  cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC  3.76 were observed to have good cross-reactivity with the epsilon-chain
CC  of IGE from cat and horse, but did not exhibit cross-reactivity with
CC  either pig or human epsilon-chains of IGE. The present sequence is the
CC  horse IGE 5.91 recognition site.
XX
XX  Sequence 15 AA;
XX
XX  Query Match 43.5%; Score 37; DB 8; Length 15;
XX  Best Local Similarity 53.8%; Pred. No. 23;
XX  Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
XX
XX  2 NDSFRTQQAATT 14
XX  |:|:|:|:|:|
XX  2 NNVLIGTDQAATT 14
XX
XX  RESULT 5
XX  ADC64568
XX  ID ADC64568 standard; peptide; 15 AA.
XX
XX  ADC64568;
XX
XX  18-DEC-2003 (first entry)
XX
XX  Horse immunoglobulin E, IGE, heavy chain immunogenic peptide P4.
XX
XX  Horse; immunoglobulin E, IGE; heavy chain; immunogen; allergy.
XX

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XX  OS Equus caballus.
XX
XX  US2003087314-A1.
XX
XX  08-MAY-2003.
XX
XX  08-NOV-2001; 2001US-00052788.
XX
XX  08-NOV-2001; 2001US-00052788.
XX
XX  08-NOV-2001; 2001US-00052788.
XX
XX  (REGC ) UNIV CALIFORNIA.
XX
XX  Gershwin LJ, Pettigrew HD, Kalina WV;
XX
XX  WPI; 2003-765437/72.
XX
XX  Immunogenic composition comprising an isolated equine immunoglobulin E
PT  polypeptide that induces production of antibodies which specifically bind
PT  to equine immunoglobulin E.
XX
XX  Example 1; Page 8; 14pp; English.
XX
XX  The invention relates to an immunogenic composition comprising an
CC  isolated polypeptide having an amino acid sequence that is at least 80%
CC  identical to 6 (S1-S6), 15 amino acid peptide sequences derived from
CC  equine immunoglobulin E (the composition induces production of an
CC  antibody that specifically binds to equine immunoglobulin (Ig)E), the six
CC  polypeptides are not explicitly identified in the specification. Also
CC  included are a composition comprising an antibody that specifically binds
CC  to a polypeptide at least 80% identical to (S1)-(S6), an antibody that
CC  specifically binds to equine IGE made by the process of immunising an
CC  animal with a polypeptide at least 80% identical to (S1)-(S6), making an
CC  antibody that specifically binds to equine IGE (involving immunising an
CC  animal with a composition further comprising an isolated polypeptide (the
CC  amino acid sequence of the polypeptide is at least 80% identical to (S1)-
CC  (S6)), and collecting antiserum from the animal) and a kit for detection
CC  of equine IGE in a biological sample comprising the antibody and means
CC  for detecting specific binding of the antibody to equine IGE. The
CC  antibody is useful for detecting equine IGE protein in a biological
CC  sample (serum) which involves contacting the sample with the antibody,
CC  thus forming an antigen/antibody complex, and detecting the presence or
CC  absence of the antigen/antibody complex. The antibody and antigen are
CC  immobilised on a solid surface. The antibody is labelled such that the
CC  complex can be detected. The complex is detected using a second labelled
CC  antibody. The peptides are useful for generating antibodies specific for
CC  IGE which can serve as a diagnostic test for allergy. The present
CC  sequence is a Horse immunoglobulin E, IGE, heavy chain immunogenic
CC  peptide from the early portion of the C4 region.
XX
XX  Sequence 15 AA;
XX
XX  Query Match 41.2%; Score 35; DB 7; Length 15;
XX  Best Local Similarity 66.7%; Pred. No. 52;
XX  Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX  6 VRTFQAATT 14
XX  |:|:|:|:|
XX  1 IOTDQAATT 9
XX
XX  RESULT 6
XX  AAU79709
XX  ID AAU79709 standard; peptide; 11 AA.
XX
XX  AAU79709;
XX
XX  15-JUL-2002 (first entry)
XX
XX  Synthetic peptide CPP-2 used in invention of DRL90.
XX
XX  Human; tissue-specific secretory polypeptide; DRU90; infection; cancer;
XX  immune disease; digestive disease; circulatory disease;
XX

```

KM endocrine disease; infertility; cytostatic; immunomodulator;  
KM antimicrobial; vasotropic; antiinfertility; hormonal; CPP-2.  
XX Synthetic.  
XX WO200224908-A1.  
XX  
XX 28-MAR-2002.  
XX  
XX 21-SEP-2001; 2001WO-JP008223.  
XX  
XX 22-SEP-2000; 2000JP-00293985.  
XX 29-SEP-2000; 2000JP-00302839.  
XX  
XX (TAKE ) TAKEDA CHEM IND LTD.  
XX  
XX Ito Y, Tanaka H, Nishimura A, Ogi K;  
PI WPI; 2002-330018/36.  
XX  
XX New tissue-specific secretory polypeptides applicable in diagnosis of and  
PT remedies for cancer, immune diseases, infection, digestive diseases,  
PT circulatory diseases, endocrine diseases and infertility.  
XX  
XX Example 8; Page 80; 11pp; Japanese.  
XX  
XX The present invention relates to the isolation of a novel tissue-specific  
CC secretory polypeptide, DRB90, and the polynucleotide sequence encoding  
CC it. The DRB90 polypeptide and encoding DNA are useful for diagnosing and  
CC treating cancer, immune diseases, infection, digestive diseases,  
CC circulatory diseases, endocrine diseases and infertility. The present  
CC sequence for synthetic peptide CPP-2 is used in the examples of the  
CC present invention  
XX  
XX  
SQ Sequence 11 AA;  
  
Query Match 37.6%; Score 32; DB 5; Length 11;  
Best Local Similarity 66.7%; Pred. No. 1.3e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 4 SPVTEQQA 12  
||: ||: ||  
Db 2 SPILTEKQA 10  
  
RESULT 7  
AAB38098  
ID AAB38098 standard; peptide; 10 AA.  
XX  
XX  
AC AAB38098;  
XX  
XX 29-JAN-2001 (first entry)  
XX  
XX Human ABC1 FHA-3 mutant exon 41-encoded peptide fragment, SEQ ID NO:65.  
DE  
XX  
XX Human ABC1 cholesterol transporter; chromosome 9q31;  
KM ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;  
KM Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;  
KM cardiovascular disease; coronary artery disease; coronary arteriosclerosis;  
KM cerebrovascular disease; peripheral vascular disease;  
KM Alzheimer's disease; Niemann-Pick disease; Huntington's disease;  
KM X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;  
KM prognosis; prophylaxis; drug screening; transgenic animal.  
XX  
XX Homo sapiens.  
XX  
XX PN WO200055318-A2.  
XX  
XX 21-SEP-2000.  
XX  
XX 15-MAR-2000; 2000WO-IB000532.  
XX  
XX 15-MAR-1999; 99US-0124702P.

PR 08-JUN-1999; 99US-0138048P.  
PR 17-JUN-1999; 99US-0139600P.  
PR 01-SEP-1999; 99US-0151977P.  
XX  
XX (UTBR-) UNIV BRITISH COLUMBIA.  
XX (XENO-) XENON BIORESEARCH INC.  
XX  
XX Hayden MR, Wilson AR, Pimstone SN;  
PI WPI; 2000-587528/55.  
XX  
XX N-PSDB; AAC69168.  
DR  
XX  
XX New ABC1 polypeptide is useful for treating diseases associated with ABC1  
PT biological activity, e.g. Alzheimer's disease, Huntington's disease and  
PT cancer.  
XX  
XX  
XX Example; Fig 6E; 229pp; English.  
XX  
XX The invention relates to the human ABC1 cholesterol transporter protein  
CC (B38082) and to nucleic acid sequences (CG9120) which encode it. ABC1 is  
CC a member of the ATP-binding cassette (ABC transporter) superfamily of  
CC proteins, and plays a crucial role in cholesterol transport, particularly  
CC intracellular cholesterol trafficking in monocytes and fibroblasts, being  
CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is  
CC located on chromosome 9q31, and mutations in this gene are associated  
CC with two genetic HDL (high density lipoprotein) deficiency disorders,  
CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases  
CC are distinguishable in that TD is an autosomal recessive disorder, while  
CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good  
CC cholesterol") in the blood correlate with a high risk of cardiovascular  
CC disease, particularly coronary artery disease, but also cerebrovascular  
CC disease, coronary arteriosclerosis, and peripheral vascular disease.  
CC Conversely, a high level of HDL has protective effects against  
CC cardiovascular disease. The invention provides genetic constructs and  
CC transgenic cells and non-human animals comprising human ABC1 nucleic  
CC acids, and methods of gene therapy for the treatment or prevention of  
CC cardiovascular disease comprising the administration of an expression  
CC vector encoding ABC1 or an active fragment thereof. The invention also  
CC encompasses compounds which mimic ABC1 activity, compounds which  
CC stimulate ABC1 expression and methods of screening for such compounds. It  
CC further relates to methods for determining whether a patient has an  
CC increased risk for cardiovascular disease due to polymorphisms in the  
CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or  
CC prevent cardiovascular disease, especially coronary artery disease,  
CC cerebrovascular disease, coronary arteriosclerosis or peripheral vascular  
CC disease. They may also be used in the treatment of diseases associated  
CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick  
CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.  
CC The invention specifically excludes proteins with the exact amino acid  
CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic  
CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The  
CC present sequence represents a human ABC1 cholesterol transporter peptide  
CC fragment used in the exemplifications of the invention  
XX  
XX  
SQ Sequence 10 AA;  
  
Query Match 35.3%; Score 30; DB 3; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2.6e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 NDSPVTEQQ 11  
||: ||: ||: ||  
Db 1 NDESVRRERQ 10  
  
RESULT 8  
AAB55476  
ID AAB55476 standard; peptide; 6 AA.  
XX  
XX  
AC AAB55476;  
XX  
XX 07-MAR-2001 (first entry)  
XX  
XX

DE Human elastase variant segment peptide SEQ ID NO:46.  
 XX Human; elastase; variant; substrate; mutant; mutagenesis; histidine;  
 KM human neutrophil elastase; H43A; cytosolic; proteolysis; ADEPT;  
 XX antibody-directed enzyme activated prodrug therapy.  
 OS Homo sapiens.  
 PN WO200068363-A2.  
 XX 16-NOV-2000.  
 PD  
 XX 04-MAY-2000; 2000WO-US006692.  
 PF  
 XX 05-MAY-1999; 99US-0132640P.  
 PR  
 XX (GETH ) GENENTECH INC.  
 PA  
 XX Carter PJ, Dall'acqua W, Rodrigues M;  
 PI WPI; 2001-007389/01.  
 DR  
 XX Elastase variant (H43A) having altered substrate specificity useful for  
 PT antibody-directed enzyme activated prodrug therapy.  
 PS Example 4; Fig 3; 79pp; English.  
 XX  
 CC The present invention describes a purified elastase variant (I) with an  
 CC amino acid sequence different from that of a precursor elastase, the  
 CC difference comprising a substitution of an active site histidine residue  
 CC corresponding to residue 43 in human neutrophil elastase with a different  
 CC amino acid residue so that (I) has substrate specificity substantially  
 CC different from the precursor elastase. (I) has cytosolic activity, and  
 CC elastase variant can be used to cleave a particular substrate, especially  
 CC those containing histidine residues at the substrate site. Site-specific  
 CC proteolysis is useful in therapeutic applications, e.g. for antibody-  
 CC directed enzyme activated prodrug therapy (ADEPT). AAC88022; AAC88023 and  
 CC AAB55432 to AAB55526 represent sequences used in the exemplification of  
 CC the present invention  
 CC  
 XX  
 SQ Sequence 6 AA;  
 QY  
 Db 10 QOATTW 15  
 1 QOATTW 6  
 Query Match 34.1%; Score 29; DB 4; Length 6;  
 Best Local Similarity 83.3%; Pred. No. 2.1e+06;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

PF 29-NOV-1993; 93WO-HU000065.  
 XX  
 XX 30-NOV-1992; 92US-00984293.  
 XX  
 XX (BIOS-) BIOSIGNAL KUTANO FEJLESZTO KFT.  
 PA (SYNT-) SYNTHETIC PEPTIDES INC.  
 XX  
 XX Kert G, Hodges RS, Cachia PJ, Szederkenyi F, Horvath A, Balogh A;  
 PI Vadasz Z;  
 PN WPI; 1994-200194/24.  
 DR  
 XX  
 XX New fatty acyl-peptide conjugates for inhibiting cell proliferation -  
 PT more active than free peptide, partic. for treating tumours, virus-  
 PT infected cells, psoriasis, etc.  
 XX  
 XX Disclosure; Fig 1; 45pp; English.  
 XX  
 CC The peptides given in AAR5718-48 can each be conjugated through an amide  
 CC linkage with a polyunsaturated fatty acid moiety, such as docosahexaenoic  
 CC acid or eicosapentaenoic acid, to improve antiproliferative activity. The  
 CC dsbDNA-dependent kinase inhibitor given in AAR5733 competes with native  
 CC kinases associated with neoplastic cell proliferation or transformation,  
 CC psoriasis, etc. (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 XX  
 SQ Sequence 15 AA;  
 QY  
 Db 1 HNDSPVRETEQ 10  
 6 YNDPMEEEE 15  
 Query Match 34.1%; Score 29; DB 2; Length 15;  
 Best Local Similarity 40.0%; Pred. No. 6.1e+02;  
 Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

RESULT 10  
 ID ADR97089 standard; peptide; 15 AA.  
 AC ADR97089;  
 DT 02-DEC-2004 (first entry)  
 XX  
 DE Cysteine protease inhibitory protein fragment #2.  
 KM antiinflammatory; vasotropic; immunostimulator;  
 KM cysteine protease inhibitory protein; diagnosis; Behcet's disease;  
 KM Harada's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2004078975-A1.  
 PD 16-SEP-2004.  
 PF 05-MAR-2004; 2004WO-JP0023902.  
 XX  
 PR 05-MAR-2003; 2003JP-00059082.  
 PA (SENP ) SENJU PHARM CO LTD.  
 XX  
 PI Katunuma N, Shiota H;  
 PN WPI; 2004-668624/65.  
 DR  
 XX Novel cysteine protease inhibitory protein, useful as diagnostic marker  
 PT for diagnosing Behcet's disease and Harada's disease.  
 PS Disclosure; SEQ ID NO 4; 64pp; Japanese.  
 CC A cysteine protease inhibitory protein (I) having the amino acid sequence  
 CC ADR97086 at its N-terminal and exhibiting the molecular weight of 31 kDa,

is new. (1) is useful for screening a compound or its salt having activity of promoting or inhibiting the function of (1). (1) enables diagnosis, prevention or treatment of Behcet's disease or Harada's disease. This sequence is a fragment of the cysteine protease inhibitory protein.

Sequence 15 AA;

Query Match 34.1%; Score 29; DB 8; Length 15;  
Best Local Similarity 38.5%; Pred. No. 6.1e+02;  
Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

3 DSPVTEQQTW 15  
3 DRPARHPEQPLW 15

RESULT 11  
AAW56548  
ID AAW56548 standard; peptide; 12 AA.

AAW56548;  
07-AUG-1998 (first entry)

Toxin fragment of Tcac of the bacterium *Photographus luminescens*.

*Photographus luminescens* W-14; nematode; symbiotic; Heterorhabdus; tca; tcd; tcc; tcd; insecticidal activity; toxin; Lepidoptera; Coleoptera; Hymenoptera; Diptera; Dictyoptera; Acarina; Homoptera; Southern; Western corn rootworm; Colorado potato beetle; mealworm; boll weevil; turf grub; beetle armyworm; black cutworm; cabbage looper; codling moth; corn earworm; European corn borer; Tobacco hornworm; budworm.

*Photographus luminescens*.

WO9808932-A1.

05-MAR-1998.

05-MAY-1997; 97WO-US007657.

28-AUG-1996; 96US-00705484.

06-NOV-1996; 96US-00743699.

06-NOV-1996; 96WO-US018003.

(DOMC) DOMELANCO.

(WISC) WISCONSIN ALUMNI RES FOUND.

Ensign JC, Bowen DJ, Petell J, Schomover S, Firench-Constant RH, Rocheleau TA, Blackburn MB, Hey TD, Merlo DJ, Orr GL, Roberts JL, Strickland JA, Guo L, Cliche TA, Sukhapiinda K;

WPI; 1998-179427/16.

Isolated toxins from *Photographus luminescens* strains - useful for control of insect pests.

Claim 30; Page 151; 32pp; English.

The present sequence represents a fragment of the toxic protein Tcac (encoded by gene tca) of the bacterium *Photographus luminescens* (W-14). This is a symbiotic bacterium of the nematodes of the Heterorhabdus genus. The bacterium has at least 4 distinct genomic regions, tca, tcd, tcc, and tcd. Peptide products are produced from these regions that are associated with insecticidal activity. The native toxins are secreted proteins. The proteins are toxic to insects upon exposure and especially when ingested. The nucleic acid sequence can be used to produce transgenic plants, baculoviruses or microbial hosts for toxin production. They can be used to control insects pests from the Lepidoptera, Coleoptera, Hymenoptera, Diptera, Dictyoptera, Acarina or Homoptera orders, especially the Southern or Western corn rootworm, Colorado potato beetle, mealworm, boll weevil, turf grub, beetle armyworm, black cutworm,

cabbage looper, codling moth, corn earworm, European corn borer or tobacco hornworm or budworm

Sequence 12 AA;

Query Match 33.5%; Score 28.5; DB 2; Length 12;  
Best Local Similarity 53.8%; Pred. No. 5.8e+02;  
Matches 7; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

3 DSPVTEQQTW 15  
3 DSP---EVSITW 12

RESULT 12  
AAW76034  
ID AAW76034 standard; protein; 9 AA.

AAW76034;

02-NOV-1998 (first entry)

LM609 grafted antibody V-L region CDR3 protein fragment #3.

Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis; primer; V-L region; CDR; complementarity determining region.

Mue sp.

WO9833919-A2.

06-AUG-1998.

30-JAN-1998; 98WO-US001826.

30-JAN-1997; 97US-00791391.

(IXSY-) IXSYS INC.

Huse WD, Glaser SM;

WPI; 1998-437472/37.

N-PSDB; AAV49871.

Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose angiogenesis or restenosis.

Claim 62; Page 41; 129pp; English.

AAW76007-W76040 are protein fragments of the grafted monoclonal antibody LM609 heavy and light chain variable region. LM609 and the antibody vitaxin bind selectively to integrin alphaVbeta3 and can be used to inhibit binding of alphaVbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphaVbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody

Sequence 9 AA;

Query Match 32.9%; Score 28; DB 2; Length 9;  
Best Local Similarity 66.7%; Pred. No. 2.1e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 10 QOATW 15  
 ||:|  
 Db 1 QOSTSW 6

## RESULT 13

AAB61392 AAB61392 standard; peptide; 9 AA.

AC AAB61392;

DT 03-APR-2001 (first entry)

DE Mutant VL CDR3 peptide #2.

KM LM609; grafted antibody; alphaVbeta\_3 integrin; angiogenesis;  
 inflammatory; cancer; retina; restenosis; osteoporosis.

OS Unidentified.

PN WO200078815-A1.

PD 28-DEC-2000.

PF 23-JUN-2000; 2000WO-US017454.

PR 24-JUN-1999; 99US-00339922.

PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

PI Huse WD, Wu H;

DR WPI; 2001-050110/06.

PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity  
 to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of  
 angiogenesis, inflammatory diseases e.g. psoriasis, cancers and  
 osteoporosis.

PS Disclosure; Page 41; 132pp; English.

CC The present invention relates to enhanced LM609 grafted antibodies  
 exhibiting selective binding affinity to alphaVbeta\_3 integrin or their  
 functional fragments. The antibodies or their functional fragments can be  
 used in the diagnosis and treatment of alphaVbeta\_3-mediated diseases  
 such as angiogenesis, inflammatory diseases (such as psoriasis and  
 chronic articular rheumatism), disorders associated with inappropriate or  
 inappropriate invasion of vessels (such as diabetic retinopathy, Kaposi's  
 neovascular glaucoma and cancer disorders such as tumours and  
 sarcoma), retinal diseases (such as macular degeneration), restenosis and  
 osteoporosis

SO Sequence 9 AA;

Query Match 32.9%; Score 28; DB 4; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 2.1e+06;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 10 QOATW 15  
 ||:|  
 Db 1 QOSTSW 6

## RESULT 14

ABO19830 ABO19830 standard; peptide; 9 AA.

AC ABO19830;

DT 28-AUG-2003 (first entry)

DE Enhanced LM609 light chain variable region CDR3 #2.

XX LM609; antibody; grafted antibody; alpha\_vbeta\_3; angiogenesis; CDR;  
 KW alpha\_vbeta\_3-mediated disease; complementarity determining region;  
 KM restenosis.

OS Unidentified.

PN US2003028009-A1.

PD 06-FEB-2003.

PF 06-JUL-2001; 2001US-00900590.

PR 30-JAN-1998; 98US-00016061.

PA (IXSY-) IXSYS INC.

PI Huse WD;

DR WPI; 2003-492042/46.

DR N-PSDB; ACD30189.

PT New Vitaxin or LM609 grafted antibody exhibiting selective binding  
 affinity to alphaVbeta3, useful for treating an alphaVbeta3-mediated  
 disease e.g., angiogenesis or restenosis.

PS Claim 65; Page 12; 71pp; English.

CC The invention relates to a Vitaxin or LM609 grafted antibody, exhibiting  
 selective binding affinity to alpha\_vbeta\_3. The Vitaxin or LM609 grafted  
 antibody is useful for treating an alpha\_vbeta\_3-mediated disease e.g.  
 angiogenesis or restenosis. The present sequence represents the amino  
 acid sequence of a LM609 complementarity determining region

SO Sequence 9 AA;

Query Match 32.9%; Score 28; DB 6; Length 9;  
 Best Local Similarity 66.7%; Pred. No. 2.1e+06;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 10 QOATW 15  
 ||:|  
 Db 1 QOSTSW 6

RESULT 15  
 ABR62303 ABR62303 standard; peptide; 9 AA.

AC ABR62303;

DT 22-SEP-2003 (first entry)

DE Surface stimulation synthetic peptide useful in HIV-1 vaccine.

KM Surface stimulation synthetic peptide; SSSP; HIV-1; vaccine; anti-HIV;

KW vitruclide; epitope.

OS Human immunodeficiency virus 1.

PN WO2003048186-A2.

PD 12-JUN-2003.

PF 23-NOV-2002; 2002WO-US037664.

PR 01-DEC-2001; 2001US-00012806.

PA (CREV/) CREVECOEUR H.

PI Crevecoeur H;

DR WPI; 2003-558941/52.

XX Configuration of synthetic peptides useful for treating hyper-variable  
PT viral pathogen e.g. HIV, involves identifying non-sequential conserved  
PT residues in selected viral proteins and designing a sequence from image  
PT scan of the residues.

XX  
PS Disclosure; Page 27; 55pp; English.

XX  
CC The present sequence is that of a surface simulation synthetic peptide  
CC (SSSP) corresponding to a non-sequential conserved residue epitope of HIV  
CC -1 glycoprotein gp120 required for viral pathogenicity. It is an example  
CC of SSSPs of the invention, which incorporate amino acid sequences that  
CC simulate the 3-dimensional spatial positions of non-sequential conserved  
CC residues necessary for viral pathogenicity. The SSSPs are useful for  
CC incorporation into vaccines effective in eliciting an effective broad  
CC spectrum immune response against hyper-variable viral pathogens such as  
CC HIV-1, and in diagnostic kits. SSSPs provide a reliable strategy for  
CC allowing the immune system to process and recognise discontinuous  
CC epitopes and to mount immune responses to the 3-dimensional  
CC configurations of targeted proteins

XX  
SQ Sequence 9 AA;

Query Match 32.9%; Score 28; DB 6; Length 9;  
Best Local Similarity 62.5%; Pred. No. 2.1e+06;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPVATEEQ 11  
: |||:|  
Db 1 NPCRTEKO 8

Search completed: May 30, 2006, 10:12:40  
Job time : 62 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 BioCeleration Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2006, 10:21:55 ; Search time 47 Seconds  
(without alignments)  
147.835 Million cell updates/sec

Title: US-10-758-165A-2  
Perfect score: 85  
Sequence: 1 HNDSPVTEQOATW 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 395127

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA Main:  
1: /EMC\_Celettera\_SIDS3/ptocdata/2/pubppaa/US07\_PUBCOMB.pep:\*  
2: /EMC\_Celettera\_SIDS3/ptocdata/2/pubppaa/US08\_PUBCOMB.pep:\*  
3: /EMC\_Celettera\_SIDS3/ptocdata/2/pubppaa/US09\_PUBCOMB.pep:\*  
4: /EMC\_Celettera\_SIDS3/ptocdata/2/pubppaa/US10A\_PUBCOMB.pep:\*  
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6: /EMC\_Celettera\_SIDS3/ptocdata/2/pubppaa/US11\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	5	US-10-758-165-2
2	48	56.5	15	5	US-10-758-165-1
3	39	45.9	15	5	US-10-758-165-7
4	37	43.5	15	5	US-10-758-165-3
5	35	41.2	15	4	US-10-052-788-4
6	32	37.6	11	4	US-10-381-089-18
7	32	37.6	15	4	US-10-381-089-8
8	30	35.3	10	4	US-10-452-510-65
9	30	35.3	10	4	US-10-617-334-65
10	30	35.3	10	4	US-10-744-465-65
11	30	35.3	10	4	US-10-833-679-65
12	30	35.3	10	5	US-10-818-279-65
13	28.5	33.5	12	4	US-10-262-794A-2
14	28	32.9	9	3	US-09-900-590-88
15	28	32.9	9	4	US-10-012-806A-39
16	28	32.9	9	4	US-10-305-231-88
17	28	32.9	9	4	US-10-463-847-88
18	28	32.9	10	4	US-10-432-234A-250
19	27	31.8	9	3	US-09-842-776A-39
20	27	31.8	9	4	US-10-239-656-31
21	27	31.8	9	4	US-10-239-656-41
22	27	31.8	9	4	US-10-467-546-21
23	27	31.8	9	5	US-10-666-332-21
24	27	31.8	9	6	US-11-108-135-12
25	27	31.8	10	6	US-11-126-978-12
26	27	31.8	10	4	US-10-432-234A-249
27	27	31.8	13	3	US-09-851-138-166

28	27	31.8	13	3	US-09-899-046-244	Sequence 244, App
29	27	31.8	13	3	US-09-878-481-244	Sequence 244, App
30	27	31.8	13	3	US-09-873-224-244	Sequence 244, App
31	27	31.8	14	5	US-10-808-187-1344	Sequence 1344, App
32	27	31.8	14	5	US-10-807-807-1344	Sequence 1344, App
33	27	31.8	14	6	US-11-004-399-2037	Sequence 2037, App
34	26	30.6	9	4	US-10-117-937-560	Sequence 560, App
35	26	30.6	9	4	US-10-428-335-103	Sequence 19, App
36	26	30.6	9	5	US-10-883-020-19	Sequence 19, App
37	26	30.6	9	6	US-11-067-064-560	Sequence 560, App
38	26	30.6	9	6	US-11-067-159-560	Sequence 560, App
39	26	30.6	9	6	US-11-203-251A-10	Sequence 10, App
40	26	30.6	9	6	US-11-203-251A-75	Sequence 75, App
41	26	30.6	10	3	US-09-908-332-53	Sequence 53, App
42	26	30.6	10	3	US-09-783-931-53	Sequence 53, App
43	26	30.6	10	4	US-10-117-937-561	Sequence 561, App
44	26	30.6	10	5	US-10-659-207-436	Sequence 436, App
45	26	30.6	10	5	US-10-929-988-436	Sequence 436, App

ALIGNMENTS

```
RESULT 1
US-10-758-165-2
; Sequence 2, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammettberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-2

Query Match      100.0%  Score 85;  DB 5;  Length 15;
Best Local Similarity 100.0%  Pred. No. 7e+08;
Matches 15;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Oy      1 HNDSPVTEQOATW 15
        |||||
Db      1 HNDSPVTEQOATW 15

RESULT 2
US-10-758-165-1
; Sequence 1, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammettberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-1

Query Match      56.5%  Score 48;  DB 5;  Length 15;
```

Best Local Similarity 61.5%; Pred. No. 0.25;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSFVTEQOATT 14  
|:|:|:|:|:  
Db 2 NDSFQTDQYTTT 14

## RESULT 3

US-10-758-165-7  
; Sequence 7, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:

; APPLICANT: Hammeberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; PRIOR FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 7  
; LENGTH: 15  
; TYPE: PRT

; ORGANISM: Sus scrofa  
US-10-758-165-7

Query Match 45.9%; Score 39; DB 5; Length 15;  
Best Local Similarity 46.2%; Pred. No. 10;  
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSFVTEQOATT 14  
|:|:|:|:|:  
Db 2 NDAFVQADRHSTT 14

## RESULT 4

US-10-758-165-3  
; Sequence 3, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:

; APPLICANT: Hammeberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165  
; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 15  
; TYPE: PRT

; ORGANISM: Equus caballus  
US-10-758-165-3

Query Match 43.5%; Score 37; DB 5; Length 15;  
Best Local Similarity 53.8%; Pred. No. 23;  
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSFVTEQOATT 14  
|:|:|:|:|:  
Db 2 NNVLQTDQOATT 14

## RESULT 5

US-10-052-788-4  
; Sequence 4, Application US/10052788  
; Publication No. US20030087314A1  
; GENERAL INFORMATION:

; APPLICANT: Gershwin, Laurel J.  
; APPLICANT: Pettigrew, Howard David

; APPLICANT: Kalina, Warren V.

; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for  
; TITLE OF INVENTION: Induction of Anti-IgE Antibodies  
; FILE REFERENCE: 023070-121000US  
; CURRENT APPLICATION NUMBER: US/10/052,788  
; CURRENT FILING DATE: 2001-11-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: epitope peptide  
; OTHER INFORMATION: P4, early portion of C4 of equine IgE epsilon  
US-10-052-788-4

Query Match 41.2%; Score 35; DB 4; Length 15;  
Best Local Similarity 66.7%; Pred. No. 51;  
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 VTEQOATT 14  
|:|:|:|:|:  
Db 1 IQTDQOATT 9

## RESULT 6

US-10-381-089-18  
; Sequence 18, Application US/10381089  
; Publication No. US20040053276A1  
; GENERAL INFORMATION:

; APPLICANT: ITO, Yasuaki  
; APPLICANT: TANAKA, Hideyuki  
; APPLICANT: NISHIMURA, Aetsushi  
; APPLICANT: OGI, Kazuhito  
; TITLE OF INVENTION: Tissue specific novel secretory polypeptide and its DNA  
; FILE REFERENCE: 2789 USOP  
; CURRENT APPLICATION NUMBER: US/10/381,089  
; CURRENT FILING DATE: 2003-03-20  
; PRIOR APPLICATION NUMBER: JP 2000-293985  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: JP 2000-302839  
; PRIOR FILING DATE: 2000-09-29  
; NUMBER OF SEQ ID NOS: 23  
; SEQ ID NO 18  
; LENGTH: 11  
; TYPE: PRT

; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide CPP1-2

US-10-381-089-18

Query Match 37.6%; Score 32; DB 4; Length 11;  
Best Local Similarity 66.7%; Pred. No. 1.2e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPVTEQQA 12  
|:|:|:|:|:  
Db 2 SPVTEKQA 10

## RESULT 7

US-10-381-089-8  
; Sequence 8, Application US/10381089  
; Publication No. US20040053276A1  
; GENERAL INFORMATION:

; APPLICANT: ITO, Yasuaki  
; APPLICANT: TANAKA, Hideyuki  
; APPLICANT: NISHIMURA, Aetsushi  
; APPLICANT: OGI, Kazuhito  
; TITLE OF INVENTION: Tissue specific novel secretory polypeptide and its DNA



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FILE REFERENCE: 2789 USOP
; CURRENT APPLICATION NUMBER: US/10/381,089
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2000-293985
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: JP 2000-302839
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human
US-10-381-089-8

Query Match      37.6%; Score 32; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
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QY 4 SPVTEQQA 12  
||: ||: ||  
1 SPILTEKQA 9

Db

RESULT 8  
US-10-452-510-65  
; Sequence 65, Application US/10452510  
; Publication No. US2004005666A1  
; GENERAL INFORMATION:  
; APPLICANT: Hayden, Michael R.  
; APPLICANT: Brooks-Wilson, Angela R.  
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS  
; FILE REFERENCE: 760050-93  
; CURRENT APPLICATION NUMBER: US/10/452,510  
; CURRENT FILING DATE: 2003-06-02  
; PRIOR APPLICATION NUMBER: US 09/526,193  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: 60/124,702  
; PRIOR FILING DATE: 1999-03-15  
; PRIOR APPLICATION NUMBER: 60/138,048  
; PRIOR FILING DATE: 1999-06-08  
; PRIOR APPLICATION NUMBER: 60/139,600  
; PRIOR FILING DATE: 1999-06-17  
; PRIOR APPLICATION NUMBER: 60/151,977  
; PRIOR FILING DATE: 1999-09-01  
; NUMBER OF SEQ ID NOS: 287  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 65  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-452-510-65

QY 2 NDSVTEQ 11  
||: ||: ||  
1 NDEVRRERQ 10

Db

Query Match 35.3%; Score 30; DB 4; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

RESULT 9  
US-10-617-334-65  
; Sequence 65, Application US/10617334  
; Publication No. US20040058869A1  
; GENERAL INFORMATION:  
; APPLICANT: Hayden, Michael R.  
; APPLICANT: Brooks-Wilson, Angela R.  
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS  
; FILE REFERENCE: 760050-91  
; CURRENT APPLICATION NUMBER: US/10/617,334  
; CURRENT FILING DATE: 2003-07-10  
; PRIOR APPLICATION NUMBER: US 09/526,193

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PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: PatentIn 3.0
; SEQ ID NO 65
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-617-334-65

Query Match      35.3%; Score 30; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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QY 2 NDSVTEQ 11  
||: ||: ||  
1 NDEVRRERQ 10

Db

RESULT 10  
US-10-744-465-65  
; Sequence 65, Application US/10744465  
; Publication No. US20040157250A1  
; GENERAL INFORMATION:  
; APPLICANT: Hayden, Michael R.  
; APPLICANT: Brooks-Wilson, Angela R.  
; APPLICANT: Plimstone, Simon N.  
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS  
; FILE REFERENCE: 760050-92  
; CURRENT APPLICATION NUMBER: US/10/744,465  
; CURRENT FILING DATE: 2003-12-23  
; PRIOR APPLICATION NUMBER: 10/617,334  
; PRIOR FILING DATE: 2003-07-10  
; PRIOR APPLICATION NUMBER: US 09/526,193  
; PRIOR FILING DATE: 2000-03-15  
; PRIOR APPLICATION NUMBER: 60/124,702  
; PRIOR FILING DATE: 1999-03-15  
; PRIOR APPLICATION NUMBER: 60/138,048  
; PRIOR FILING DATE: 1999-06-08  
; PRIOR APPLICATION NUMBER: 60/139,600  
; PRIOR FILING DATE: 1999-06-17  
; PRIOR APPLICATION NUMBER: 60/151,977  
; PRIOR FILING DATE: 1999-09-01  
; NUMBER OF SEQ ID NOS: 287  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 65  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-744-465-65

QY 2 NDSVTEQ 11  
||: ||: ||  
1 NDEVRRERQ 10

Db

RESULT 11  
US-10-833-679-65  
; Sequence 65, Application US/10833679  
; Publication No. US20040185508A1  
; GENERAL INFORMATION:  
; APPLICANT: Hayden, Michael R.

APPLICANT: Brooks-Wilson, Angela R.  
APPLICANT: Pimstone, Simon N.  
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS  
FILE REFERENCE: 760050-135  
CURRENT FILING DATE: 2004-04-28  
PRIOR APPLICATION NUMBER: 10/452,510  
PRIOR FILING DATE: 2003-06-02  
PRIOR APPLICATION NUMBER: 10/617,334  
PRIOR FILING DATE: 2003-07-10  
PRIOR APPLICATION NUMBER: 09/526,193  
PRIOR FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: 60/124,702  
PRIOR FILING DATE: 1999-03-15  
PRIOR APPLICATION NUMBER: 60/138,048  
PRIOR FILING DATE: 1999-06-08  
PRIOR APPLICATION NUMBER: 60/139,600  
PRIOR FILING DATE: 1999-06-17  
PRIOR APPLICATION NUMBER: 60/151,977  
PRIOR FILING DATE: 1999-09-01  
NUMBER OF SEQ ID NOS: 287  
SOFTWARE: PatentIn 3.0  
SEQ ID NO 65  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-833-679-65

Query Match 35.3%; Score 30; DB 4; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 NDSVPRTEQ 11  
Db 1 NDEDVRRERQ 10

RESULT 12  
US-10-818-279-65  
Sequence 65, Application US/10818279  
Publication No. US20050136421A1  
GENERAL INFORMATION:  
APPLICANT: Hayden, Michael R.  
APPLICANT: Brooks-Wilson, Angela R.  
APPLICANT: Pimstone, Simon N.  
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS  
FILE REFERENCE: 760050-126  
CURRENT APPLICATION NUMBER: US/10/818,279  
CURRENT FILING DATE: 2004-04-05  
PRIOR APPLICATION NUMBER: 10/745,377  
PRIOR FILING DATE: 2003-12-23  
PRIOR APPLICATION NUMBER: 10/617,334  
PRIOR FILING DATE: 2003-07-10  
PRIOR APPLICATION NUMBER: 09/526,193  
PRIOR FILING DATE: 2000-03-15  
PRIOR APPLICATION NUMBER: 60/124,702  
PRIOR FILING DATE: 1999-03-15  
PRIOR APPLICATION NUMBER: 60/138,048  
PRIOR FILING DATE: 1999-06-08  
PRIOR APPLICATION NUMBER: 60/139,600  
PRIOR FILING DATE: 1999-06-17  
PRIOR APPLICATION NUMBER: 60/151,977  
PRIOR FILING DATE: 1999-09-01  
NUMBER OF SEQ ID NOS: 287  
SOFTWARE: PatentIn 3.0  
SEQ ID NO 65  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-818-279-65

Query Match 35.3%; Score 30; DB 5; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2.5e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
OY 2 NDSVPRTEQ 11  
Db 1 NDEDVRRERQ 10

RESULT 13  
US-10-262-794A-2  
Sequence 2, Application US/10262794A  
Publication No. US2003020786A1  
GENERAL INFORMATION:  
APPLICANT: Ensigen, Jerald C  
APPLICANT: Bowen, David J  
APPLICANT: Petell, James  
APPLICANT: Fatig, Raymond  
APPLICANT: Schoonover, Sue  
APPLICANT: French-Constant, Richard  
APPLICANT: Rocheleau, Thomas A.  
APPLICANT: Blackburn, Michael B.  
APPLICANT: Hey, Timothy D.  
APPLICANT: Merlo, Donald J.  
APPLICANT: Orr, Gregory L.  
APPLICANT: Roberts, Jean L.  
APPLICANT: Strickland, James A.  
APPLICANT: Guo, Lining  
APPLICANT: Cliche, Todd A.  
APPLICANT: Sukhupinda, Kitieri  
TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dow Agrosciences Patent Department  
STREET: 9330 Zionsville Road  
CITY: Indianapolis  
STATE: IN  
COUNTRY: US  
ZIP: 46268  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: IBM PC compatible  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/262,794A  
FILING DATE: 02-OCT-2002  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/851,567  
FILING DATE: 05-MAY-1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/063,615  
FILING DATE: 18-MAY-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/395,497  
FILING DATE: 28-FEB-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/007,255  
FILING DATE: 06-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/608,423  
FILING DATE: 28-FEB-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/705,484  
FILING DATE: 28-AUG-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J  
REGISTRATION NUMBER: 27386  
REFERENCE/DOCKET NUMBER: 960296,93804  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 608-251-5000  
TELEFAX: 608-251-9166  
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:  
LENGTH: 12 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: N-terminal  
US-10-262-794A-2

Query Match 33.5%; Score 28.5; DB 4; Length 12;  
Best Local Similarity 53.8%; Pred. No. 5.7e+02;  
Matches 7; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 3 DSPVTEQQTW 15  
DB 3 DSP---EVSITW 12

RESULT 14  
US-09-900-590-88

; Sequence 88, Application US/09900590  
; Publication No. US20030028009A1  
; GENERAL INFORMATION:

APPLICANT: Huse, William D.

GLAER, Scott M.

TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human

Antibodies, Nucleic Acids Encoding Same and Methods of Use

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/900,590

FILING DATE: 06-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/016,061

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-IX 2965

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 88:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 88:

US-09-900-590-88

Query Match 32.9%; Score 28; DB 3; Length 9;

Best Local Similarity 66.7%; Pred. No. 1.9e+06;

Matches 4; Conservative 2; Mismatches 0; Indels 0;

QY 10 QOATW 15  
DB 1 QOATW 6

RESULT 15

US-10-012-806A-39

; Sequence 39, Application US/10012806A

; Publication No. US20030125518A1

; GENERAL INFORMATION:

APPLICANT: CREVICOUER, HARRY

TITLE OF INVENTION: SURFACE SIMULATION SYNTHETIC PEPTIDES USEFUL IN THE

TREATMENT OF HYPER-VARIABLE VIRAL PATHOGENS

FILE REFERENCE: 2001-Crev1

CURRENT APPLICATION NUMBER: US/10/012,806A

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patent Ver. 2.1

SEQ ID NO 39

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-012-806A-39

Query Match 32.9%; Score 28; DB 4; Length 9;

Best Local Similarity 62.5%; Pred. No. 1.9e+06;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPVTEQ 11  
DB 1 NPCRTERQ 8

Search completed: May 30, 2006, 10:24:41

Job time : 48 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 30, 2006, 10:22:25 ; Search time 5.66667 Seconds  
(without alignments)  
29.481 Million cell updates/sec

Title: US-10-758-165a-2

Sequence: 1 HNDSPVTEQATW 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 10973

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA New:  
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2: /EMC\_Celerra\_SIDS3/prodata/1/pubppa/US06\_NEW\_PUB.pap:\*  
3: /EMC\_Celerra\_SIDS3/prodata/1/pubppa/US07\_NEW\_PUB.pap:\*  
4: /EMC\_Celerra\_SIDS3/prodata/1/pubppa/US08\_NEW\_PUB.pap:\*  
5: /EMC\_Celerra\_SIDS3/prodata/1/pubppa/PCT\_NEW\_PUB.pap:\*  
6: /EMC\_Celerra\_SIDS3/prodata/1/pubppa/US10\_NEW\_PUB.pap:\*  
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8: /EMC\_Celerra\_SIDS3/prodata/1/pubppa/US60\_NEW\_PUB.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	31.8	9	US-11-297-317-21	Sequence 21, App1
2	26	30.6	9	US-11-140-487A-1220	Sequence 1220, App
3	25	29.4	14	US-11-122-986-778	Sequence 778, App
4	23	27.1	10	US-10-538-066-163	Sequence 163, App
5	22	25.9	7	US-10-489-071-6	Sequence 6, App1
6	22	25.9	11	US-10-546-594-92	Sequence 92, App1
7	21	24.7	9	US-11-140-487A-1766	Sequence 1766, App
8	21	24.7	10	US-10-516-079-64	Sequence 64, App1
9	20	23.5	9	US-11-023-959A-63	Sequence 63, App1
10	20	23.5	11	US-10-981-300-34	Sequence 34, App1
11	20	23.5	12	US-11-106-014-84	Sequence 84, App1
12	20	23.5	15	US-11-140-487A-2207	Sequence 2207, App
13	19	22.4	8	US-10-538-066-404	Sequence 404, App
14	19	22.4	9	US-10-538-066-159	Sequence 159, App
15	19	22.4	9	US-10-538-066-429	Sequence 429, App
16	19	22.4	9	US-11-023-959A-18	Sequence 18, App1
17	19	22.4	9	US-11-023-959A-36	Sequence 36, App1
18	19	22.4	9	US-11-023-959A-51	Sequence 51, App1
19	19	22.4	9	US-11-023-959A-72	Sequence 72, App1
20	19	22.4	9	US-11-332-378-76	Sequence 76, App1
21	19	22.4	10	US-10-538-066-184	Sequence 184, App
22	19	22.4	10	US-10-538-066-268	Sequence 268, App
23	19	22.4	10	US-10-538-066-413	Sequence 413, App
24	19	22.4	10	US-10-538-066-415	Sequence 415, App
25	19	22.4	11	US-10-538-066-393	Sequence 393, App

26	19	22.4	11	6	US-10-538-066-414	Sequence 414, App
27	19	22.4	12	6	US-10-538-066-381	Sequence 381, App
28	19	22.4	13	7	US-11-121-382-197	Sequence 197, App
29	19	22.4	15	7	US-11-140-487A-2231	Sequence 2231, App
30	18	21.2	6	6	US-10-525-126-33	Sequence 33, App1
31	18	21.2	7	6	US-10-522-043-2	Sequence 2, App1
32	18	21.2	8	7	US-11-213-668-74	Sequence 74, App1
33	18	21.2	9	6	US-10-538-066-174	Sequence 174, App
34	18	21.2	9	6	US-10-538-066-299	Sequence 299, App
35	18	21.2	9	6	US-11-140-487A-895	Sequence 895, App
36	18	21.2	9	7	US-11-140-487A-1042	Sequence 1042, App
37	18	21.2	9	7	US-11-140-487A-1377	Sequence 1377, App
38	18	21.2	9	7	US-11-140-487A-1561	Sequence 1561, App
39	18	21.2	9	7	US-11-140-487A-1767	Sequence 1767, App
40	18	21.2	10	6	US-10-489-266-20	Sequence 20, App1
41	18	21.2	10	6	US-10-538-066-172	Sequence 172, App
42	18	21.2	10	6	US-10-538-066-267	Sequence 267, App
43	18	21.2	10	7	US-11-140-487A-1378	Sequence 1378, App
44	18	21.2	10	7	US-11-140-487A-1768	Sequence 1768, App
45	18	21.2	10	7	US-11-140-487A-1869	Sequence 1869, App

#### ALIGNMENTS

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RESULT 1
US-11-297-317-21
Sequence 21, Application US/11297317
Publication No. US20060088525A1
GENERAL INFORMATION:
APPLICANT: Gregorio Aversa
APPLICANT: Frank Kolbinger
APPLICANT: Jose M. Carballido Herrera
APPLICANT: Andras Aszodi
APPLICANT: Jose W. Saldenha
APPLICANT: Bruce M. Hall
TITLE OF INVENTION: Therapeutic binding molecules
FILE REFERENCE: Not Yet Known
CURRENT APPLICATION NUMBER: US/11/297,317
CURRENT FILING DATE: 2005-12-08
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 21
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial
NAME/KEY: MISC FEATURE
FEATURE:
OTHER INFORMATION: hypervariable region CDR3' in a CD45RO/RB binding molecule of SEQ
US-11-297-317-21
Query Match
Best Local Similarity 31.8%; Score 27; DB 7; Length 9;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy 10 QOATW 15
Db 1 QOSNTW 6
RESULT 2
US-11-140-487A-1220
Sequence 1220, Application US/11140487A
Publication No. US20060093617A1
GENERAL INFORMATION:
APPLICANT: Immunogenetics N.V.
TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C v.l.
FILE REFERENCE: 166
CURRENT APPLICATION NUMBER: US/11/140,487A
CURRENT FILING DATE: 2005-05-31
PRIORITY APPLICATION NUMBER: EP 04012951.2
PRIORITY FILING DATE: 2004-06-01

```

PRIOR APPLICATION NUMBER: EP 04447239.7  
PRIOR FILING DATE: 2004-10-28  
PRIOR APPLICATION NUMBER: EP 05102441.2  
PRIOR FILING DATE: 2005-03-25  
PRIOR APPLICATION NUMBER: US 60/576,310  
PRIOR FILING DATE: 2004-06-03  
PRIOR APPLICATION NUMBER: US 60/622,782  
PRIOR FILING DATE: 2004-10-29  
PRIOR APPLICATION NUMBER: US 60/665,395  
PRIOR FILING DATE: 2005-03-25  
NUMBER OF SEQ ID NOS: 2278  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1220  
LENGTH: 9  
TYPE: PRT  
ORGANISM: hepatitis C virus  
US-11-140-487A-1220

Query Match 30.6%; Score 26; DB 7; Length 9;  
Best Local Similarity 80.0%; Pred. No. 5.2e+04;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 HNDSP 5  
Db 1 HNDSP 5

RESULT 3  
US-11-122-986-778  
Sequence 778, Application US/11122986  
Publication No. US20060104989A1  
GENERAL INFORMATION:  
APPLICANT: EDWARDS, ALED  
APPLICANT: DHARMSI, AKIL  
APPLICANT: VEDADI, MASOUD  
TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES  
FILE REFERENCE: IPT-330.01  
CURRENT APPLICATION NUMBER: US/11/122,986  
PRIOR FILING DATE: 2005-05-05  
PRIOR APPLICATION NUMBER: 60/423,875  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: 60/423,832  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: 60/423,915  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: 60/423,757  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: 60/423,758  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: 60/424,367  
PRIOR FILING DATE: 2002-11-06  
PRIOR APPLICATION NUMBER: 60/424,376  
PRIOR FILING DATE: 2002-11-06  
PRIOR APPLICATION NUMBER: 60/424,370  
PRIOR FILING DATE: 2002-11-06  
PRIOR APPLICATION NUMBER: 60/424,362  
PRIOR FILING DATE: 2002-11-06  
PRIOR APPLICATION NUMBER: 60/424,373  
PRIOR FILING DATE: 2002-11-06  
Remainig Prior Application data removed - See File wrapper or PALM.  
NUMBER OF SEQ ID NOS: 844  
SOFTWARE: PatentIn Ver. 3.3  
SEQ ID NO 778  
LENGTH: 14  
TYPE: PRT  
ORGANISM: Staphylococcus aureus  
US-11-122-986-778

Query Match 29.4%; Score 25; DB 7; Length 14;  
Best Local Similarity 42.9%; Pred. No. 92;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 HNDSPVR 7

Db 8 HSDTRPAK 14

RESULT 4  
US-10-538-066-163  
Sequence 163, Application US/10538066  
Publication No. US20060094649A1  
GENERAL INFORMATION:  
APPLICANT: EpiImmune Inc.  
TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen  
FILE REFERENCE: 2060.015PC06  
CURRENT APPLICATION NUMBER: US/10/538,066  
CURRENT FILING DATE: 2005-06-09  
PRIOR APPLICATION NUMBER: US 60/432,017  
PRIOR FILING DATE: 2002-12-10  
NUMBER OF SEQ ID NOS: 767  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 163  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-538-066-163

Query Match 27.1%; Score 23; DB 6; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 DSPVPT 8  
Db 3 DSPVPT 8

RESULT 5  
US-10-489-071-6  
Sequence 6, Application US/10489071  
Publication No. US20060094672A1  
GENERAL INFORMATION:  
APPLICANT: PASQUALINE ET AL.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST  
FILE REFERENCE: UTSC:856US  
CURRENT APPLICATION NUMBER: US/10/489,071  
CURRENT FILING DATE: 2004-03-08  
PRIOR APPLICATION NUMBER: PCT/US02/27836  
PRIOR FILING DATE: 2002-08-30  
NUMBER OF SEQ ID NOS: 144  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 6  
LENGTH: 7  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Peptide  
US-10-489-071-6

Query Match 25.9%; Score 22; DB 6; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.2e+04;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 DSPVR 7  
Db 3 DSPVR 7

RESULT 6  
US-10-546-594-92  
Sequence 92, Application US/10546594  
Publication No. US20060088538A1  
GENERAL INFORMATION:  
APPLICANT: HOSOKAWA, Saiko  
APPLICANT: AOKI, Masehiko

APPLICANT: HIRAKAWA, Yoko  
APPLICANT: ITRMT, Seima  
APPLICANT: UMEKI, Hiroe  
APPLICANT: SAIKAWA, Yoshiro  
APPLICANT: KUMAI, Koichiro  
APPLICANT: FUKUDA, Kazumasa  
TITLE OF INVENTION: MONOCLONAL ANTIBODY AND GENE ENCODING THE SAME, HYBRIDOMA, PHARM  
FILE REFERENCE: 238067  
CURRENT APPLICATION NUMBER: US/10/546,594  
CURRENT FILING DATE: 2005-08-19  
PRIOR APPLICATION NUMBER: JP 2003/54670  
PRIOR FILING DATE: 2003-02-28  
PRIOR APPLICATION NUMBER: JP 2003/194643  
PRIOR FILING DATE: 2003-07-09  
NUMBER OF SEQ ID NOS: 132  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 92  
LENGTH: 11  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-546-594-92

Query Match 25.9%; Score 22; DB 6; Length 11;  
Best Local Similarity 33.3%; Pred. No. 2.4e+02;  
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 RTEQARTW 15  
DB 1 RASQSISW 9

RESULT 7  
US-11-140-487A-1766  
Sequence 1766, Application US/11140487A  
Publication No. US20060093617A1  
GENERAL INFORMATION:  
APPLICANT: Immunogenetics N.V.  
TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi  
FILE REFERENCE: 166  
CURRENT APPLICATION NUMBER: US/11/140,487A  
CURRENT FILING DATE: 2005-05-31  
PRIOR APPLICATION NUMBER: EP 04012951.2  
PRIOR FILING DATE: 2004-06-01  
PRIOR APPLICATION NUMBER: EP 04447239.7  
PRIOR FILING DATE: 2004-10-28  
PRIOR APPLICATION NUMBER: EP 05102441.2  
PRIOR FILING DATE: 2005-03-25  
PRIOR APPLICATION NUMBER: US 60/576,310  
PRIOR FILING DATE: 2004-06-03  
PRIOR APPLICATION NUMBER: US 60/622,782  
PRIOR FILING DATE: 2004-10-29  
PRIOR APPLICATION NUMBER: US 60/665,395  
PRIOR FILING DATE: 2005-03-25  
NUMBER OF SEQ ID NOS: 2278  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1766  
LENGTH: 9  
TYPE: PRT  
ORGANISM: hepatitis C virus  
US-11-140-487A-1766

Query Match 24.7%; Score 21; DB 7; Length 9;  
Best Local Similarity 57.1%; Pred. No. 5.2e+04;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 SPVTEQ 10  
DB 1 SPLTTNQ 7

RESULT 8  
US-10-516-079-64

Sequence 64, Application US/10516079  
Publication No. US20060088699A1  
GENERAL INFORMATION:  
APPLICANT: ALVAREZ, Vernon L.  
APPLICANT: GRIMES, Carol A.  
APPLICANT: GONDA, Matthew A.  
TITLE OF INVENTION: Combination chemotherapy with chlorotoxin  
FILE REFERENCE: 51530-5006-WO  
CURRENT APPLICATION NUMBER: US/10/516,079  
CURRENT FILING DATE: 2004-11-29  
PRIOR APPLICATION NUMBER: US 60/406,033  
PRIOR FILING DATE: 2002-08-27  
PRIOR APPLICATION NUMBER: US 60/384,171  
PRIOR FILING DATE: 2002-05-31  
NUMBER OF SEQ ID NOS: 95  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 64  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: Pep21-SCX8\_LEIQH sequence  
US-10-516-079-64

Query Match 24.7%; Score 21; DB 6; Length 10;  
Best Local Similarity 66.7%; Pred. No. 3.2e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 TEQOAT 13  
DB 2 TDQGMT 7

RESULT 9  
US-11-023-959A-63  
Sequence 63, Application US/11023959A  
Publication No. US20060106203A1  
GENERAL INFORMATION:  
APPLICANT: Winter, Greg  
TITLE OF INVENTION: Ligand  
FILE REFERENCE: 8039/2142  
CURRENT APPLICATION NUMBER: US/11/023,959A  
CURRENT FILING DATE: 2004-12-28  
PRIOR APPLICATION NUMBER: PCT/GB03/002804  
PRIOR FILING DATE: 2003-06-30  
NUMBER OF SEQ ID NOS: 187  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 63  
LENGTH: 9  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-11-023-959A-63

Query Match 23.5%; Score 20; DB 7; Length 9;  
Best Local Similarity 50.0%; Pred. No. 5.2e+04;  
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 QOARTW 15  
DB 1 QOGARW 6

RESULT 10  
US-10-981-300-34  
Sequence 34, Application US/10981300  
Publication No. US20060093599A1  
GENERAL INFORMATION:  
APPLICANT: GADIGAZIT-BORNSTEIN  
TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS  
FILE REFERENCE: ABGX-005  
CURRENT APPLICATION NUMBER: US/10/981,300

;; CURRENT FILING DATE: 2004-11-03  
;; NUMBER OF SEQ ID NOS: 71  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 34  
;; LENGTH: 11  
;; TYPE: PRT  
;; ORGANISM: homo sapiens  
US-10-961-300-34

Query Match 23.5%; Score 20; DB 6; Length 11;  
Best Local Similarity 33.3%; Pred. No. 5.3e+02;  
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 RTEQATTW 15  
DB 1 RASQGISW 9

RESULT 11

US-11-106-014-84  
; Sequence 84, Application US/11106014  
; Publication No. US20060088846A1  
; GENERAL INFORMATION:  
; APPLICANT: Pagano, Michele  
; APPLICANT: Chlaui, Dah Sharim  
; APPLICANT: Latres, Esther  
; APPLICANT: Srivastava, Promod  
; APPLICANT: Chandawarkar, Rajiv  
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT  
; TITLE OF INVENTION: OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS  
; FILE REFERENCE: 5914-106-999  
; CURRENT APPLICATION NUMBER: US/11/106,014  
; CURRENT FILING DATE: 2005-04-13  
; PRIOR APPLICATION NUMBER: 10/632,150  
; PRIOR FILING DATE: 2003-07-30  
; PRIOR APPLICATION NUMBER: 10/042,417  
; PRIOR FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: 09/385,219  
; PRIOR FILING DATE: 1999-08-27  
; PRIOR APPLICATION NUMBER: 60/118,568  
; PRIOR FILING DATE: 1999-02-03  
; PRIOR APPLICATION NUMBER: 60/098,355  
; PRIOR FILING DATE: 1998-08-28  
; PRIOR APPLICATION NUMBER: 60/124,449  
; PRIOR FILING DATE: 1997-03-15  
; NUMBER OF SEQ ID NOS: 96  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 84  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-106-014-84

Query Match 23.5%; Score 20; DB 7; Length 12;  
Best Local Similarity 44.4%; Pred. No. 5.8e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 DSPVTEQO 11  
DB 3 EAQVRKENQ 11

RESULT 12

US-11-140-487A-2207  
; Sequence 2207, Application US/11140487A  
; Publication No. US20060093617A1  
; GENERAL INFORMATION:  
; APPLICANT: Innogenetics N.V.  
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi  
; FILE REFERENCE: 166  
; CURRENT APPLICATION NUMBER: US/11/140,487A  
; CURRENT FILING DATE: 2005-05-31  
; PRIOR APPLICATION NUMBER: EP 04012951.2

;; PRIOR FILING DATE: 2004-06-01  
;; PRIOR APPLICATION NUMBER: EP 04447239.7  
;; PRIOR FILING DATE: 2004-10-28  
;; PRIOR APPLICATION NUMBER: EP 05102441.2  
;; PRIOR FILING DATE: 2005-03-25  
;; PRIOR APPLICATION NUMBER: US 60/576,310  
;; PRIOR FILING DATE: 2004-06-03  
;; PRIOR APPLICATION NUMBER: US 60/622,782  
;; PRIOR FILING DATE: 2004-10-29  
;; PRIOR APPLICATION NUMBER: US 60/665,395  
;; PRIOR FILING DATE: 2005-03-25  
;; NUMBER OF SEQ ID NOS: 2278  
;; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2207  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: hepatitis C virus  
US-11-140-487A-2207

Query Match 23.5%; Score 20; DB 7; Length 15;  
Best Local Similarity 44.4%; Pred. No. 7.3e+02;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 SPVTEQQA 12  
DB 2 SPVFTDNSS 10

RESULT 13

US-10-538-066-404  
; Sequence 404, Application US/10538066  
; Publication No. US20060094649A1  
; GENERAL INFORMATION:  
; APPLICANT: Epiimmune Inc.  
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen  
; TITLE OF INVENTION: Peptides and Compositions  
; FILE REFERENCE: 2060.01SPC06  
; CURRENT APPLICATION NUMBER: US/10/538,066  
; CURRENT FILING DATE: 2005-06-09  
; PRIOR APPLICATION NUMBER: US 60/432,017  
; PRIOR FILING DATE: 2002-12-10  
; NUMBER OF SEQ ID NOS: 767  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 404  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-538-066-404

Query Match 22.4%; Score 19; DB 6; Length 8;  
Best Local Similarity 57.1%; Pred. No. 5.2e+04;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 EQQATTW 15  
DB 2 EAQNTTY 8

RESULT 14

US-10-538-066-159  
; Sequence 159, Application US/10538066  
; Publication No. US20060094649A1  
; GENERAL INFORMATION:  
; APPLICANT: Epiimmune Inc.  
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen  
; TITLE OF INVENTION: Peptides and Compositions  
; FILE REFERENCE: 2060.01SPC06  
; CURRENT APPLICATION NUMBER: US/10/538,066  
; CURRENT FILING DATE: 2005-06-09  
; PRIOR APPLICATION NUMBER: US 60/432,017  
; PRIOR FILING DATE: 2002-12-10  
; NUMBER OF SEQ ID NOS: 767  
; SOFTWARE: PatentIn version 3.2



; SEQ ID NO 159  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-538-066-159

Query Match 22.4%; Score 19; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 5.2e+04;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QOAT 13  
|||  
Db 1 QOAT 4

RESULT 15  
US-10-538-066-429  
; Sequence 429, Application US/10538066  
; Publication No. US20060094649A1  
; GENERAL INFORMATION:  
; APPLICANT: Epiimmune Inc.  
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen  
; FILE REFERENCE: 2060.015PC06  
; CURRENT APPLICATION NUMBER: US/10/538,066  
; CURRENT FILING DATE: 2005-06-09  
; PRIOR APPLICATION NUMBER: US 60/432,017  
; PRIOR FILING DATE: 2002-12-10  
; NUMBER OF SEQ ID NOS: 767  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 429  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-538-066-429

Query Match 22.4%; Score 19; DB 6; Length 9;  
Best Local Similarity 57.1%; Pred. No. 5.2e+04;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 EQOATW 15  
|||  
Db 2 EAQNTTY 8

Search completed: May 30, 2006, 10:25:03  
Job time : 5.66667 secs

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GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 30, 2006, 09:58:50 ; Search time 60 Seconds  
(without alignments)  
114.304 Million cell updates/sec

Title: US-10-758-165A-1  
Sequence: 1 RNDSPITQDQYTTTG 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 837128

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_8:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*  
9: geneseqp2005s:\*  
10: geneseqp2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	100.0	15	8	ADRI0601 Dog IGE e
2	53	65.4	15	8	ADRI0607 Pig IGE e
3	48	59.3	15	8	ADRI0602 Cat IGE e
4	41	50.6	15	8	ADRI0603 Horse IGE
5	34	42.0	15	7	ADCG4568 Horse imm
6	32	39.5	10	5	ABG98754 F protein
7	32	39.5	10	5	ABG98755 F protein
8	32	39.5	11	2	AA79898 Fusion pr
9	31	38.3	14	2	AAW35339 Rat GDNF
10	31	38.3	14	2	AAW84178 Rat GDNF
11	31	38.3	15	4	AEC98667 HLA-DR bi
12	30	37.0	14	4	AAW98177 Human pep
13	30	37.0	14	9	AED12588 Anti-Notog
14	29	35.8	10	3	AAV51451 AAV VP3 d
15	29	35.8	10	4	AAW46909 AAV mutan
16	29	35.8	10	8	ADG94454 Human JAM
17	29	35.8	10	8	AD146852 Permeabil
18	29	35.8	10	8	ADP87029 Junctiona
19	29	35.8	15	8	ADRI0604 Sheep IGE
20	28	34.6	8	7	ADJ72341 Streptomy
21	28	34.6	8	8	ADG94478 Human JAM
22	28	34.6	8	8	AD146877 Permeabil
23	28	34.6	8	8	ADP87053 Junctiona

24	28	34.6	10	6	ABJ19566 Neuronal
25	28	34.6	10	8	ABY01523 SARS coro
26	28	34.6	10	8	ADY01210 SARS coro
27	28	34.6	10	9	ADZ86156 SARS coro
28	28	34.6	10	9	AA45250 Apolipop
29	28	34.6	14	4	AAE05129 Peptide #
30	28	34.6	15	9	ADV51735 SARS-COV
31	28	34.6	15	9	ADV51737 SARS-COV
32	28	34.6	15	9	ADV51734 SARS-COV
33	28	34.6	15	9	ADV51736 SARS-COV
34	28	34.6	15	9	ADV51733 SARS-COV
35	28	34.6	15	9	ADV51739 SARS-COV
36	28	34.6	15	9	ADV51743 SARS-COV
37	28	34.6	15	9	ADV51738 SARS-COV
38	28	34.6	15	9	ADV51740 SARS-COV
39	28	34.6	15	9	ADV51741 SARS-COV
40	28	34.6	15	9	ADV51742 SARS-COV
41	27	33.3	9	9	ADW23315 SARS coro
42	27	33.3	9	9	ADW23210 SARS coro
43	27	33.3	9	9	ADW23329 SARS coro
44	27	33.3	9	9	AEC97896 HLA-A24-b
45	27	33.3	10	5	ABG98753 F protein

## ALIGNMENTS

RESULT 1  
ID ADRI0601 standard; peptide; 15 AA.  
AC ADRI0601;  
DT 21-OCT-2004 (first entry)  
XX Dog IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.  
DE  
XX Antiaethmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.  
XX  
XX Canis familiaris.  
OS  
XX WO2004065936-A2.  
PN  
XX  
XX 05-AUG-2004.  
PD  
XX 15-JAN-2004; 2004WO-US003566.  
PF  
XX 16-JAN-2003; 2003US-0440472P.  
PR  
XX (UYNC-) UNIV NORTH CAROLINA STATE.  
PA  
XX Hammerberg B;  
PI  
XX WPI: 2004-593545/57.  
XX  
XX Novel antibody that specifically binds to mammalian IGE epitope, useful  
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
or treating asthma or anaphylactic shock.  
XX  
XX Example 6; Page 9; 14pp; English.  
PS  
XX The present invention relates to a novel monoclonal antibody (I) that  
XX specifically binds to a mammalian IGE epitope, where the epitope is  
XX between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
XX (I) is useful for testing an allergen reactivity of an IGE sample. The  
XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
XX and corn allergens. The sample is a biological sample collected from a  
XX dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
XX antibodies recognise epitopes on canine IGE corresponding to amino acid  
XX residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
XX canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE.

XX Sequence 15 AA;

Query Match 100.0%; Score 81; DB 8; Length 15;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RNDSPQTQDYTTTG 15  
 |||||  
 Db 1 RNDSPQTQDYTTTG 15

RESULT 2

ADRI0607  
 ID ADRI0607 standard; peptide; 15 AA.

XX ADRI0607;

XX 21-OCT-2004 (first entry)

XX Pig IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 7.

XX Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
 KW pig.

XX Sus scrofa.

XX WO2004065936-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.

XX (UNNC-) UNIV NORTH CAROLINA STATE.

XX Hammerberg B;

XX WPI; 2004-593545/57.

XX Novel antibody that specifically binds to mammalian IGE epitope, useful  
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IGE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC pig IGE 5.91 recognition site.

XX Sequence 15 AA;

Query Match 65.4%; Score 53; DB 8; Length 15;  
 Best Local Similarity 57.1%; Pred. No. 0.044;

Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RNDSPQTQDYTTT 14  
 |||||  
 Db 1 RNDAPVQADRHSTT 14

RESULT 3

ADRI0602  
 ID ADRI0602 standard; peptide; 15 AA.

XX ADRI0602;

XX 21-OCT-2004 (first entry)

XX Cat IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.

XX Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
 KW cat.

XX Felis catus.

XX WO2004065936-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.

XX (UNNC-) UNIV NORTH CAROLINA STATE.

XX Hammerberg B;

XX WPI; 2004-593545/57.

XX Novel antibody that specifically binds to mammalian IGE epitope, useful  
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IGE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the  
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC cat IGE 5.91 recognition site.

XX Sequence 15 AA;

Query Match 59.3%; Score 48; DB 8; Length 15;  
 Best Local Similarity 61.5%; Pred. No. 0.33;  
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 2 NDSPQTQDYTTT 14  
 |||||  
 Db 2 NDSPVTEQOATTT 14

RESULT 4  
 ADRI0603

ID ADR10603 standard; peptide: 15 AA.  
 XX  
 AC ADR10603;  
 XX  
 DT 21-OCT-2004 (first entry)  
 XX  
 DE Horse IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 3.  
 XX  
 KW Antischematic; Antiallergic; Immunosuppressive; IGE; dog; asthma;  
 KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;  
 XX horse.  
 OS Equus caballus.  
 XX  
 PN WO2004065936-A2.  
 XX  
 PD 05-AUG-2004.  
 XX  
 PF 15-JAN-2004; 2004NO-US003566.  
 XX  
 PR 16-JAN-2003; 2003US-0440472P.  
 XX  
 PA (UYNC-) UNIV NORTH CAROLINA STATE.  
 XX  
 PI Hammerberg B;  
 XX  
 DR WPI; 2004-593545/57.  
 XX  
 PT Novel antibody that specifically binds to mammalian IGE epitope, useful  
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE  
 PT or treating asthma or anaphylactic shock.  
 PS  
 XX Example 6; Page 9; 14pp; English.  
 XX  
 CC The present invention relates to a novel monoclonal antibody (I) that  
 CC specifically binds to a mammalian IGE epitope, where the epitope is  
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.  
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The  
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut  
 CC and corn allergens. The sample is a biological sample collected from a  
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for  
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal  
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid  
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the  
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from  
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and  
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain  
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with  
 CC either pig or human epsilon-chains of IGE. The present sequence is the  
 CC horse IGE 5.91 recognition site.  
 XX  
 SQ Sequence 15 AA;  
 XX  
 Query Match 50.6%; Score 41; DB 8; Length 15;  
 Best Local Similarity 64.3%; Pred. No. 5.4;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 RNDSPIDQYTTT 14  
 ||: ||||| ||  
 Db 1 RNNVLIQTDQATT 14  
 ||: ||||| ||  
 RESULT 5  
 ADR64568  
 ID ADR64568 standard; peptide: 15 AA.  
 XX  
 AC ADR64568;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide P4.  
 XX  
 KW Horse; immunoglobulin E; IGE; heavy chain; immunogen; allergy.

XX  
 OS Equus caballus.  
 XX  
 PN US2003087314-A1.  
 XX  
 DT 08-MAY-2003.  
 XX  
 DE 08-NOV-2001; 2001US-00052788.  
 XX  
 PR 08-NOV-2001; 2001US-00052788.  
 XX  
 PA (REGC) UNIV CALIFORNIA.  
 XX  
 PI Gershwin LJ, Pettigrew HD, Kalina WV;  
 XX  
 DR WPI; 2003-765437/72.  
 XX  
 PT Immunogenic composition comprising an isolated equine immunoglobulin E  
 PT polypeptide that induces production of antibodies which specifically bind  
 PT to equine immunoglobulin E.  
 PS  
 XX Example 1; Page 8; 14pp; English.  
 XX  
 CC The invention relates to an immunogenic composition comprising an  
 CC isolated polypeptide having an amino acid sequence that is at least 80%  
 CC identical to 6 (S1-S6), amino acid peptide sequences derived from  
 CC equine immunoglobulin E (the composition induces production of an  
 CC antibody that specifically binds to equine immunoglobulin (Ig)E, the six  
 CC polypeptides are not explicitly identified in the specification. Also  
 CC included are a composition comprising an antibody that specifically binds  
 CC to a polypeptide at least 80% identical to (S1)-(S6), an antibody that  
 CC specifically binds to equine IGE made by the process of immunising an  
 CC animal with a polypeptide at least 80% identical to (S1)-(S6), making an  
 CC antibody that specifically binds to equine IGE (involving immunising an  
 CC animal with a composition further comprising an isolated polypeptide (the  
 CC amino acid sequence of the polypeptide is at least 80% identical to (S1)-  
 CC (S6)), and collecting antiserum from the animal) and a kit for detection  
 CC of equine IGE in a biological sample comprising the antibody and means  
 CC for detecting specific binding of the antibody to equine IGE. The  
 CC antibody is useful for detecting equine IGE protein in a biological  
 CC sample (serum) which involves contacting the sample with the presence or  
 CC absence of an antigen/antibody complex, and detecting the presence or  
 CC absence of the antigen/antibody complex. The antibody and antigen are  
 CC immobilised on a solid surface. The antibody is labelled such that the  
 CC complex can be detected. The complex is detected using a second labelled  
 CC antibody. The peptides are useful for generating antibodies specific for  
 CC IGE which can serve as a diagnostic test for allergy. The present  
 CC sequence is a Horse immunoglobulin E, IGE, heavy chain immunogenic  
 CC peptide from the early portion of the C4 region.  
 XX  
 SQ Sequence 15 AA;  
 XX  
 Query Match 42.0%; Score 34; DB 7; Length 15;  
 Best Local Similarity 77.8%; Pred. No. 89;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 6 IQTDQYTTT 14  
 ||||| ||  
 Db 1 IQTDQYTTT 9  
 ||||| ||  
 RESULT 6  
 ABG98754  
 ID ABG98754 standard; peptide: 10 AA.  
 XX  
 AC ABG98754;  
 XX  
 DT 13-JAN-2003 (first entry)  
 XX  
 DE F protein decapeptide #241.  
 XX  
 KW F protein; RSV; decapeptide; negative sense single stranded RNA virus;  
 KW viral F protein; F protein mediated host cell virion fusion; virucide;

KW F protein mediated host cell virion budding.  
 XX  
 OS Respiratory syncytial virus.  
 XX  
 PN WO200242326-A1.  
 XX  
 PD 30-MAY-2002.  
 XX  
 PF 22-NOV-2001, 2001WO-AU001517.  
 XX  
 PR 22-NOV-2000, 2000US-0252767P.  
 XX  
 PR  
 PA (BIOT-) BIOTA SCI MANAGEMENT PTY LTD.  
 XX  
 XX  
 PI Mason AJ, Tucker SP, Young PR;  
 XX  
 XX WPI; 2002-599372/64.  
 DR  
 XX  
 PT Facilitating production of a protein for analyzing, designing and/or  
 PT modifying an agent that can interact with a viral F protein, comprises  
 PT expressing a nucleic acid optimized for expression of the protein, using  
 PT a eukaryotic cell.  
 XX  
 XX  
 PS Claim 42; Page 102; 367pp; English.

The invention relates to a method for facilitating production of a protein or its derivative from a negative sense single stranded RNA virus, by expressing a nucleic acid molecule encoding the protein in a host cell, where the nucleic acid is optimised for expression by a eukaryotic cell. The protein, especially F protein, is useful for analysing, designing and/or modifying an agent capable of interacting with a viral F protein or its derivative and modulating a functional activity associated with the protein, by contacting the protein with a putative agent and assessing the degree of interactive complementarity of the agent with the protein. An optimised nucleic acid or its derivative, equivalent, analogue or mimetic is useful for interacting with a viral F protein and modulating a functional activity associated with the viral protein, for use in the manufacture of a medicament utilised in the therapeutic and/or prophylactic treatment of conditions characterised by infection with a negative sense single stranded RNA virus, and for modulating a functional activity associated with a viral F protein in a subject, preferably a mammal, especially a human, where the functional activity is F protein mediated host cell virion fusion and/or virion budding and the modulating is down regulation. Sequences ABG96514-ABG99058 represent F protein decapetptides of the invention

Sequence 10 AA:

Query Match	39.5%	Score 32;	DB 5;	Length 10;
Best Local Similarity	66.7%;	Pred. No. 1.3e+02;		
Matches 6; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY	2	NDSP	IQTDQ	10
Db	2	NDMP	ITNDQ	10

RESULT 7  
ABG98755  
ID ABG98755 standard: peptide: 10 AA.

AC ABG98755

DT 13-JAN-2003 (first entry)

DE F protein decapeptide #242.

KW F protein; RSV; decapeptide; negative sense single stranded RNA virus;

KW F protein mediated host cell virion budding.

Respiratory syncytial virus.

yy

PN	WO200242326-A1.
XX	
PD	30-MAY-2002.
XX	
PF	22-NOV-2001; 2001WO-AU001517.
XX	
PR	22-NOV-2000; 2000US-0252767P.
XX	
PA	(BIOT-) BIOTA SCI MANAGEMENT PTY LTD.
XX	
PI	Mason AJ, Tucker SP, Young PR;
XX	
DR	WPI; 2002-599372/64.
XX	
PT	Facilitating production of a protein for analyzing, designing and/or
PT	modifying an agent that can interact with a viral P protein, comprises
PT	expressing a nucleic acid optimized for expression of the protein, using
PT	a eukaryotic cell.

PS Claim 42; Page 102; 367pp; English.

The invention relates to a method for facilitating production of a protein or its derivative from a negative sense single stranded RNA virus, by expressing a nucleic acid molecule encoding the protein in a host cell, where the nucleic acid is optimised for expression by a eukaryotic cell. The protein, especially F protein, is useful for analysing, designing and/or modifying an agent capable of interacting with a viral F protein or its derivative and modulating a functional activity associated with the protein, by contacting the protein with a putative agent and assessing the degree of interactive complementarity of the agent with the protein. An optimised nucleic acid or its derivative, equivalent, analogue or mimetic is useful for interacting with a viral F protein and modulating a functional activity associated with the viral protein, for use in the manufacture of a medicament utilised in the therapeutic and/or prophylactic treatment of conditions characterised by infection with a negative sense single stranded RNA virus, and for modulating a functional activity associated with a viral F protein in a subject, preferably a mammal, especially a human, where the functional activity is F protein mediated host cell fusion and/or virion budding and the modulating is down regulation. Sequences ABG38514-ABG39058 represent F protein decoy peptides of the invention.

AA Sequence 10 AA;  
SQ

Query Match	39.5%	Score 32;	DB 5;	Length 10;
Best Local Similarity	66.7%;	Pred. No. 1.3e+02;		
Matches 6; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0.

QY 2 NDSPIQT DQ 10  
|||  
Db 1 NDMPI TNDQ 9

RESULT 8  
AAR79898  
ID AAR79898 standard; peptide; 13 AA.

AC AAR

AA 25-MAR-20  
DT

[illegible]

XX DE  
DE

XXXXXXXXXXXXXXXXXXXX

KW human; therapy; diagnosis; immunoassay.

OS Synthetic.

PN CA1336955-C.

PD 12-SEP-1995.

27

PF 20-SEP-1989; 89CA-00612131.  
XX 20-SEP-1988; 88US-00247017.  
PR 20-SEP-1989; 89US-00409915.  
XX (PRAXIS-) PRAXIS BIOLOGICS INC.  
PA  
XX Paradoiso PR, Hu BT, Arnumugham R, Hildreth SW, Martin-Gallardo A,  
PI Welsh EE;  
DR WPI; 1995-328674/43.  
XX  
PT Sub-unit vaccine against respiratory syncytial virus - contains  
PT polypeptide related to neutralising epitope on G protein, opt. also  
PT polypeptide from F protein.  
XX  
XX Disclosure; Fig 3; 119pp; English.  
XX  
CC The sequences represented by AAR79895-R79899 are synthetic peptides  
CC corresponding to regions of the respiratory syncytial (RS) virus fusion  
CC protein (see AAR79894). This sequence corresponds to residues 261-273.  
CC These fragments were used to create antibodies. The DNA encoding these  
CC fragments is inserted into expression vectors and used to transform cell  
CC cultures, the expressed protein is then isolated and purified. These  
CC peptide fragments are then used in a vaccine. Alternatively, the  
CC antibodies against these fragments could be used to confer short-term  
CC protection against the RS virus. The vaccine can then be used to protect  
CC humans and animals (for animals, the RS sequence used is from the RS  
CC virus of that species). The dose of the vaccine is 0.1-100 micro grammes  
CC per kg body weight. The vaccine can also be used in diagnosis, such as  
CC immunoassays. The DNA encoding this sequence can be used in hybridisation  
CC tests to detect RS virus in blood. The antibodies can be used to identify  
CC viral epitopes. The advantage with using this methodology is that there  
CC is no enhancement/potentiation of the disease seen with current  
CC treatments. (Updated on 25-MAR-2003 to correct PF field.)  
CC  
XX  
SQ Sequence 13 AA:  
Query Match 39.5%; Score 32; DB 2; Length 13;  
Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 NDSPIQTDQ 10  
DB 2 NDMPTINDQ 10  
RESULT 9  
AAW5339  
ID AAW35339 standard; peptide; 14 AA.  
XX  
AC AAW35339;  
XX  
DT 01-MAY-1998 (first entry)  
XX  
DE Rat GDNF receptor residues 356-369.  
XX  
XX Rat; glial cell line-derived neurotrophic factor; GDNF; receptor;  
KM treatment; dopaminergic nerve cell disorder; Parkinson's disease;  
KM Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;  
KM Huntington's disease; glaucoma; retinal degeneration; hearing loss;  
KM gene therapy.  
XX  
OS Rattus sp.  
XX  
PN W09740152-A1.  
XX  
PD 30-OCT-1997.  
XX  
PF 15-APR-1997; 97WO-US006281.  
XX  
PR 22-APR-1996; 96US-0015907P.  
PR 09-MAY-1996; 96US-0017221P.

BR 14-APR-1997; 97US-00837199.  
XX  
XX (AMGEN-) AMGEN INC.  
PA  
XX Fox GM, Wen D, Jing S;  
PI  
XX WPI; 1997-535836/49.  
DR  
XX  
PT Glial cell line derived neurotrophic factor receptor - useful to treat  
PT dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's  
PT disease.  
XX  
XX Disclosure; Page 21; 196pp; English.  
XX  
CC The present peptide is derived from rat glial cell line-derived  
CC neurotrophic factor (GDNF) receptor, which can be used to treat  
CC dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's  
CC disease or amyotrophic lateral sclerosis, complications of diabetes and  
CC Huntington's disease and (optionally in combination with GDNF) glaucoma,  
CC retinal degeneration and hearing loss caused by injury to inner ear  
CC sensory neurons. The receptor can also be used to block unwanted GDNF  
CC activity, analyse GDNF related molecules and stabilise GDNF in  
CC pharmaceutical formulations. Receptor expressing cells, preferably  
CC transfected ex vivo, can be used similarly by implantation, and the use  
CC of the receptor cDNA in gene therapy is also contemplated. Probes based  
CC on the cDNA can be used to identify GDNF responsive cells and tissues,  
CC e.g. to identify patients who would benefit from GDNF therapy, and  
CC abnormalities in receptor expression, and to isolate molecules that form  
CC a complex with the cDNA or are homologous/cross-reactive with the cDNA.  
CC Anti-receptor antibodies, oligonucleotides derived from the cDNA and  
CC animal models that overexpress the receptor can be used to study the  
CC biological function of GDNF, knockout transgenic animals can be used to  
CC detect GDNF dependent neurons or processes and the antibody can be used  
CC in immunoassays for the receptor. The receptor binds GDNF specifically  
CC and with high affinity, acting as part of a complex that  
CC mediates/enhances signal transduction by GDNF, i.e. increasing dopamine  
CC uptake in dopaminergic cells  
CC  
XX  
SQ Sequence 14 AA:  
Query Match 38.3%; Score 31; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 2.8e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 5 PIQTDQYTTT 14  
DB 4 PVQTTRATTT 13  
RESULT 10  
AAW84178  
ID AAW84178 standard; peptide; 14 AA.  
XX  
AC AAW84178;  
XX  
DT 25-MAR-1999 (first entry)  
XX  
DE Rat GDNFR-alpha derived peptide.  
XX  
XX Rat; glial cell line derived neurotrophic factor receptor-alpha;  
KM GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;  
KM neuritin; signal transduction; dopaminergic nerve cell;  
KM Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;  
KM neurological disorder; diabetes; glaucoma; sensory neuron;  
KM retinal ganglion cell degeneration; sensory neuropathy; retinopathy;  
KM gene therapy.  
XX  
OS Synthetic.  
XX  
PN Rattus sp.  
XX  
PD W09854213-A2.  
XX  
XX 03-DEC-1998.

```

XX 27-APR-1998; 98WO-US008486.
XX
XX 30-MAY-1997; 97US-00866354.
XX
XX (AMGE-) AMGEN INC.
XX
XX Fox GM, Jing S, Wen D,
XX
XX WPI; 1999-080806/07.
XX
XX New isolated glial cell line-derived neurotrophic factor receptors - used
XX to develop products for treating e.g. improperly functioning dopaminergic
XX nerve cells, Parkinson's disease, Alzheimer's disease or amyotrophic
XX lateral sclerosis.
XX
XX Disclosure; Page 24; 318pp; English.
XX
XX The present peptide is derived from rat glial cell-line derived
XX neurotrophic factor receptor-alpha (GDNFR-alpha) amino acids 356-369. It
XX is used to raise antibodies against GDNFR-alpha. The peptide may also
XX possess an activity of GDNFR-alpha. The GDNFR-alpha protein is capable of
XX complexing with glial cell line-derived neurotrophic factor (GDNF) and
XX mediating cell response to GDNF. GDNFR-alpha proteins are functionally,
XX characterised by the ability to bind GDNF and/or neuritin specifically,
XX and to act as part of a molecular complex which mediates or enhances the
XX signal transduction affects of GDNF and/or neuritin. The proteins can be
XX used for treating improperly functioning dopaminergic nerve cells,
XX Parkinson's disease, Alzheimer's disease or amyotrophic lateral
XX sclerosis. They can also be used for treating neurological disorders
XX associated with diabetes, glaucoma or other diseases and conditions
XX involving retinal ganglion cell degeneration, sensory neuropathy caused
XX by injury to, insults to, or degeneration of, sensory neurons,
XX pathological conditions, or disease or injury-related neuropathies. The
XX products can also be used for detection, diagnosis, drug screening and
XX gene therapy
XX
XX Sequence 14 AA;
XX
XX Query Match 38.3%; Score 31; DB 2; Length 14;
XX Best Local Similarity 60.0%; Pred. No. 2.8e+02;
XX Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX 5 PIOTDQYTTT 14
XX |:|||
XX 4 PVQTTTATT 13
XX
XX RESULT 11
XX AEC98667
XX ID AEC98667 standard; peptide; 15 AA.
XX
XX AEC98667;
XX
XX 01-DEC-2005 (first entry)
XX
XX HLA-DR binding epitope from HPV E2 protein #156.
XX
XX Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;
XX epitope mapping; immune stimulation; cytotoxic T-lymphocyte;
XX human leukocyte antigen.
XX
XX Human papillomavirus.
XX
XX WO2005089164-A2.
XX
XX 29-SEP-2005.
XX
XX 03-JAN-2005; 2005WO-US000077.
XX
XX 31-DEC-2003; 2003US-0533211P.
XX
XX 02-JUL-2004; 2004US-0584652P.
XX

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PA (EPIM-) EPIMUNE INC.
PA (INNO-) INNOGENETICS NV.
PA (CHES/) CHESNUT R.
PA (NEMM/) NEMMAN M J.
PA (MOTH/) MOTH B.
PA (BAKE/) BAKER D.
PA (SOUT/) SOUTHOOD S.
PA (BABE/) BABE L M.
PA (CHEN/) CHEN Y.
PA (DEYO/) DEYOUNG L M.
PA (HUAN/) HUANG M T F.
PA (POME/) POWER S D.
PI Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;
PI Chen Y, Deyoung LM, Huang MTF, Power SD;
XX
XX WPI; 2005-658982/67.
XX
XX New polynucleotide comprises a multi-epitope construct comprising nucleic
XX acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte
XX (CTL) epitopes, useful in preparing a vaccine against HPV.
XX
XX Disclosure; Page 333; 518pp; English.
XX
XX The invention relates to a new polynucleotide comprising a multi-epitope
XX construct comprising nucleic acids encoding the human papillomavirus
XX (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16 E1,214, and that
XX are directly or indirectly joined to one another in the same reading
XX frame, a vaccine multigene. Also included are a vector comprising the
XX multi-epitope construct, a polypeptide comprising an amino acid sequence
XX encoded by the polynucleotide, a composition (comprising the
XX polynucleotide, vector and/or polypeptide and a carrier), a cell
XX (comprising the polynucleotide, vector or polypeptide), inducing an
XX immune response against human papillomavirus virus (HPV), and making the
XX polynucleotide, vector or polypeptide. The epitopes are derived from
XX different strains of HPV and are from the E1, E2, E6 and E7 proteins. The
XX epitopes may be linked via a GP-anchor/spacer peptide. The order of the
XX epitopes in the vaccine protein are disclosed in the tables referred to
XX in the claims of the specification. The polynucleotide, vector or
XX polypeptide is useful in preparing a composition for inducing an immune
XX response against human papillomavirus virus (HPV) and thus providing a
XX defense against HPV infection and HPV-related cancers. The present
XX sequence is an HPV-derived peptide epitope that binds to a subclass of
XX human leukocyte antigen (HLA) peptides.
XX
XX Sequence 15 AA;
XX
XX Query Match 38.3%; Score 31; DB 9; Length 15;
XX Best Local Similarity 55.6%; Pred. No. 3e+02;
XX Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
XX 4 SPIOTDQYT 12
XX |:||:|
XX 2 SPYRTDEWT 10
XX
XX Db
XX
XX RESULT 12
XX AAM98177
XX ID AAM98177 standard; peptide; 14 AA.
XX
XX AAM98177;
XX
XX 24-JAN-2002 (first entry)
XX
XX Human peptide #1452 encoded by a SNP oligonucleotide.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
XX amyloid protein; angiopoietin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinesin; cytokine; interferon;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX

```



KM nervous system disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200147944-A2.  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 28-DEC-2000; 2000WO-US035498.  
 XX  
 PR 28-DEC-1999; 99US-0173419P.  
 XX 27-DEC-2000; 2000US-00173419.  
 PA (CURA-) CURAGEN CORP.  
 PI Shimkets RA, Leach M;  
 PS WPI; 2001-465210/50.  
 XX  
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,  
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,  
 PT autoimmune diseases and infections.  
 XX  
 PS Disclosure; Page 3986; 4143pp; English.  
 XX  
 CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)  
 CC encoding polymorphic variants of proteins related to amylases, amyloid  
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,  
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,  
 CC complement related proteins, cytochromes, kinesins, cytokines,  
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.  
 CC The present sequence is a peptide encoded by one such oligonucleotide.  
 CC The oligonucleotides and the peptides encoded by them may be used in the  
 CC prevention, diagnosis and treatment of diseases associated with  
 CC inappropriate expression of the proteins listed above. Disorders that may  
 CC be prevented, diagnosed and/or treated include multifactorial diseases  
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid  
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus  
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,  
 CC brain, breast, colon and kidney, leukemia), diseases of the nervous  
 CC system and an infection of pathogenic organisms  
 XX  
 SQ Sequence 14 AA;  
 Query Match 37.0%; Score 30; DB 4; Length 14;  
 Best Local Similarity 55.6%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 Oy 6 IQTQDYTTT 14  
 :|||:|:  
 Db 5 VQTDKVTST 13  
 RESULT 13  
 AED12588  
 ID AED12588 standard; peptide: 14 AA.  
 XX  
 AC AED12588;  
 XX  
 DT 01-DEC-2005 (first entry)  
 XX  
 DE Anti-Nogor scFv protein NCF0121 HC CDR3 sequence.  
 KM Neuroprotective; Vulnerary; Vasotropic; Cerebroprotective;  
 KM spinal cord injury; brain injury; paralysis; neurodegenerative disease;  
 KM cerebrovascular ischemia; Nogo receptor; Nogor.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2005215770-A1.  
 XX  
 PD 29-SEP-2005.  
 XX

PF 25-MAR-2005; 2005US-00090847.  
 XX  
 PR 26-MAR-2004; 2004US-0556386P.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Bell A, Rosen CA;  
 XX  
 DR WPI; 2005-648835/66.  
 XX  
 PT New antibody or its fragment that specifically binds Nogo receptor  
 PT (Nogor), useful in preparing a composition for treating or ameliorating  
 PT spinal cord injury, brain trauma, paralysis, neurodegenerative disorders  
 PT or stroke.  
 XX  
 PS Example 1; Page 69; 81pp; English.  
 XX  
 CC The present invention relates to a novel antibody or its fragment (e.g.  
 CC an scFv) that binds to the Nogo receptor (Nogor; AED12284). The antibody  
 CC comprises a Variable Heavy Complementarity Determining Region (VHCDR1),  
 CC VHCDR2 or VHCDR3 and a Variable Light Complementarity Determining Region  
 CC (VLCDR1, VLCDR2 or VLCDR3). The antibody prevents binding or inhibits  
 CC interaction of Nogor with: p75(NTR) (AED12288); LINGO-1 (AED12289); Nogo  
 CC (AED12285); OMgp (AED12286); or MAG (AED12287), and promotes neurite  
 CC outgrowth or axonal regeneration. The antibody is useful in preparing a  
 CC composition for treating or ameliorating spinal cord injury, brain  
 CC trauma, paralysis, neurodegenerative disorders or stroke. The present  
 CC sequence is a CDR peptide sequence for one such scFv that binds to Nogor.  
 XX  
 SQ Sequence 14 AA;  
 Query Match 37.0%; Score 30; DB 9; Length 14;  
 Best Local Similarity 45.5%; Pred. No. 4.1e+02;  
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;  
 Oy 5 PIQTQDYTTT 15  
 :|||:|:  
 Db 1 PLSDYDTSG 11  
 RESULT 14  
 AAY51451  
 ID AAY51451 standard; peptide: 10 AA.  
 XX  
 AC AAY51451;  
 XX  
 DT 11-MAY-2000 (first entry)  
 XX  
 DE AAV VP3 derived peptide fragment #6.  
 XX  
 KM VP3; structural protein; capsid; tropism; diagnosis; gene therapy.  
 XX  
 OS Adeno-associated virus.  
 XX  
 PN WO9967393-A2.  
 XX  
 PD 29-DEC-1999.  
 XX  
 PF 21-JUN-1999; 99WO-EP004288.  
 XX  
 PR 19-JUN-1998; 98DE-01027457.  
 XX  
 PA (MED1-) MEDIGENE AG.  
 XX  
 PI Hallek M, Ried M, Deleage G, Girod A;  
 XX  
 DR WPI; 2000-160586/14.  
 XX  
 PT Structure proteins of adeno-associated virus with at least one mutation  
 PT have increased infectiveness.  
 XX  
 PS Example 2; Page 42; 43pp; German.  
 XX

CC This invention describes novel structural proteins of adeno-associated  
CC virus (AAV) especially AAV-capsids with at least one mutation and which  
CC have an increased infectiveness. The structural proteins are used to  
CC alter the tropism of AAV, to transform cells, for diagnosis and for  
CC effectively studies for gene therapy and/or for genomic targeting.  
CC AAV51446-Y51467 represent AAV derived peptides used to illustrate the  
CC method of the invention

XX  
SQ Sequence 10 AA;

Query Match 35.8%; Score 29; DB 3; Length 10;  
Best Local Similarity 50.0%; Pred. No. 4.3e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 SPIQTDQY 11  
: : : : :  
Db 1 NPVATEQY 8

#### RESULT 15

AA046909  
ID AAB46909 standard; peptide; 10 AA.

XX  
AC AAB46909;

XX  
DT 04-MAY-2001 (first entry)

XX  
DE AAV mutant VP3 derived peptide SEQ ID 14.

XX  
KW VP3 protein; structural protein; chromatography; tropism; antigenicity;  
KW genomic targeting; gene therapy; purification; affinity tag.

XX  
OS Adeno associated virus.

XX  
PN DE19933719-A1.

XX  
PD 25-JAN-2001.

XX  
PF 19-JUL-1999; 99DE-01033719.

XX  
PR 19-JUL-1999; 99DE-01033719.

XX  
PA (MEDI-) MEDIGENE AG.

XX  
PI Hallek M, Girod A, Ried M, Koerner C;

XX  
DR WPI; 2001-203661/21.

XX  
PT New mutant adeno-associated virus structural protein with altered  
PT chromatographic properties, useful in preparation of gene therapy  
PT vectors.

XX  
PS Example 1; Page 15; 20pp; German.

XX  
CC This invention describes a novel structural protein (I) of adeno-  
CC associated virus (AAV) which has at least one mutation that alters the  
CC chromatographic properties of the virus. The invention also describes (1)  
CC a nucleic acid (II) that encodes (I); (2) a cell (III) containing (II);  
CC and (3) producing (I) comprising culturing (III). (I), (II) and (III) are  
CC used to purify AAV and its particles, to alter the tropism or  
CC antigenicity of AAV, to transform cells, for genomic targeting, for  
CC diagnosis, for examination of activity and/or gene therapy. Altering the  
CC chromatographic properties improves purification, especially  
CC concentration of virus and produces viral particles to a higher titre or  
CC higher purity and/or provides more efficient purification (fewer steps,  
CC and a quicker and less expensive process). Particularly, mutated (I)  
CC result in viruses that are eluted at a different (higher or lower) salt  
CC concentration than the wild type, which tends to co-elute with other  
CC viruses, serum proteins and cellular debris, or that include a specific  
CC affinity tag. Mutation may also allow targeting of cells, e.g.  
CC hematopoietic cells, that are not normally targets for AAV

XX  
SQ Sequence 10 AA;

Query Match 35.8%; Score 29; DB 4; Length 10;  
Best Local Similarity 50.0%; Pred. No. 4.3e+02;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 SPIQTDQY 11  
: : : : :  
Db 1 NPVATEQY 8

Search completed: May 30, 2006, 10:12:43  
Job time : 61 secs

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## OM protein - protein search, using sw model

Run on: May 30, 2006, 10:21:55 ; Search time 47 Seconds

(without alignments)  
147.835 Million cell updates/sec

Title: US-10-758-165A-1

Sequence: 1 RNDSPIDTDYTTTG 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 395127

Minimum DB seq length: 0  
Maximum DB seq length: 15Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

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1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	5	US-10-758-165-1
2	53	65.4	15	5	US-10-758-165-7
3	48	59.3	15	5	US-10-758-165-2
4	41	50.6	15	5	US-10-758-165-3
5	34	42.0	15	4	US-10-052-788-4
6	32	39.5	10	4	US-10-432-234A-249
7	32	39.5	10	4	US-10-432-234A-250
8	31	38.3	14	4	US-10-155-693-29
9	31	38.3	14	5	US-10-872-161-29
10	29	35.8	10	4	US-10-462-452-433
11	29	35.8	10	4	US-10-601-953-561
12	29	35.8	10	4	US-10-322-266-434
13	29	35.8	12	3	US-09-990-832C-108
14	29	35.8	15	5	US-10-758-165-4
15	28	34.6	8	4	US-10-462-452-457
16	28	34.6	8	4	US-10-601-953-586
17	28	34.6	8	4	US-10-322-266-458
18	28	34.6	10	5	US-10-475-049A-24
19	28	34.6	10	5	US-10-936-237-18
20	28	34.6	11	4	US-10-378-173-28
21	27	33.3	10	4	US-10-281-479A-27
22	27	33.3	10	4	US-10-275-180A-27
23	27	33.3	10	4	US-10-286-132A-27
24	27	33.3	10	4	US-10-432-234A-248
25	27	33.3	13	5	US-10-948-707-846
26	27	33.3	13	5	US-10-948-707-949
27	27	33.3	15	4	US-10-080-608A-161

28	27	33.3	15	4	US-10-370-465-70	Sequence 70, Appl
29	26	32.1	9	4	US-10-428-115-103	Sequence 103, App
30	26	32.1	10	3	US-09-572-404B-1728	Sequence 1728, App
31	26	32.1	10	4	US-10-149-138-543	Sequence 543, App
32	26	32.1	10	4	US-10-149-138-1265	Sequence 1265, App
33	26	32.1	10	4	US-10-149-138-1902	Sequence 1902, App
34	26	32.1	10	4	US-10-149-138-543	Sequence 543, App
35	26	32.1	10	4	US-10-149-138-1265	Sequence 1265, App
36	26	32.1	10	4	US-10-149-138-1902	Sequence 1902, App
37	26	32.1	10	4	US-10-432-234A-251	Sequence 251, App
38	26	32.1	10	5	US-10-475-049A-15	Sequence 15, Appl
39	26	32.1	12	4	US-10-078-968-5	Sequence 5, Appl
40	26	32.1	12	4	US-10-279-991-13	Sequence 13, Appl
41	26	32.1	13	5	US-10-948-707-1324	Sequence 1324, App
42	26	32.1	14	3	US-09-826-230-126	Sequence 126, App
43	26	32.1	14	4	US-10-264-309-71	Sequence 71, Appl
44	26	32.1	14	5	US-10-264-309-71	Sequence 71, Appl
45	26	32.1	14	5	US-10-530-061-2185	Sequence 2185, App

## ALIGNMENTS

```
RESULT 1
US-10-758-165-1
; Sequence 1, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammeberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-1

Query Match      100.0%; Score 81; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RNDSPIDTDYTTTG 15
DB      1 RNDSPIDTDYTTTG 15

RESULT 2
US-10-758-165-7
; Sequence 7, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammeberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-758-165-7

Query Match      65.4%; Score 53; DB 5; Length 15;
```

Best Local Similarity 57.1%; Pred. No. 0.039; DB 5; Length 15;  
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNDSPQOTDQYTTT 14  
|||:|:|:|:|  
Db 1 RNDAPVQADRHSTT 14

## RESULT 3

US-10-758-165-2  
; Sequence 2, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:

APPLICANT: Hammerberg, Bruce  
TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
FILE REFERENCE: 5051-661  
CURRENT APPLICATION NUMBER: US/10/758.165  
CURRENT FILING DATE: 2004-01-16  
PRIOR APPLICATION NUMBER: US 60/440,472  
PRIOR FILING DATE: 2003-01-16  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Felis catus

US-10-758-165-2

Query Match 59.3%; Score 48; DB 5; Length 15;  
Best Local Similarity 61.5%; Pred. No. 0.29;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQOTDQYTTT 14  
|||:|:|:|:|  
Db 2 NDSPIQOTDQYTTT 14

## RESULT 4

US-10-758-165-3  
; Sequence 3, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:

APPLICANT: Hammerberg, Bruce  
TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
FILE REFERENCE: 5051-661  
CURRENT APPLICATION NUMBER: US/10/758.165  
CURRENT FILING DATE: 2004-01-16  
PRIOR APPLICATION NUMBER: US 60/440,472  
PRIOR FILING DATE: 2003-01-16  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 3  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Equus caballus

US-10-758-165-3

Query Match 50.6%; Score 41; DB 5; Length 15;  
Best Local Similarity 64.3%; Pred. No. 4.7;  
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNDSPQOTDQYTTT 14  
|||:|:|:|:|  
Db 1 RNDAPVQADRHSTT 14

## RESULT 5

US-10-052-788-4  
; Sequence 4, Application US/10052788  
; Publication No. US2003008731A1  
; GENERAL INFORMATION:

APPLICANT: Gerishwin, Laurel J.  
APPLICANT: Pettigrew, Howard David

APPLICANT: Kalina, Warren V.  
TITLE OF INVENTION: The Regents of the University of California  
TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for  
FILE REFERENCE: 023070-121000US  
CURRENT APPLICATION NUMBER: US/10/052.788  
CURRENT FILING DATE: 2001-11-08  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 15  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: epitope peptide  
OTHER INFORMATION: P4, early portion of C4 of equine IgE epsilon  
US-10-052-788-4

Query Match 42.0%; Score 34; DB 4; Length 15;  
Best Local Similarity 77.8%; Pred. No. 76;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 IQTDQYTTT 14  
|||:|:|:|:|  
Db 1 IQTDQYTTT 9

## RESULT 6

US-10-432-234A-249  
; Sequence 249, Application US/10432234A  
; Publication No. US20040161846A1  
; GENERAL INFORMATION:

APPLICANT: Biocr Scientific Management Pty Ltd  
TITLE OF INVENTION: A method of expression and agents identified thereby  
FILE REFERENCE: 12084720/TDO  
CURRENT APPLICATION NUMBER: US/10/432.234A  
CURRENT FILING DATE: 2003-05-22  
PRIOR APPLICATION NUMBER: US 60/252767  
PRIOR FILING DATE: 2000-11-22  
NUMBER OF SEQ ID NOS: 574  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 249  
LENGTH: 10  
TYPE: PRT  
ORGANISM: respiratory syncytial virus  
US-10-432-234A-249

Query Match 39.5%; Score 32; DB 4; Length 10;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIQTDQ 10  
|||:|:|:|:|  
Db 2 NDSPIQTDQ 10

US-10-432-234A-250  
; Sequence 250, Application US/10432234A  
; Publication No. US20040161846A1  
; GENERAL INFORMATION:

APPLICANT: Biocr Scientific Management Pty Ltd  
TITLE OF INVENTION: A method of expression and agents identified thereby  
FILE REFERENCE: 12084720/TDO  
CURRENT APPLICATION NUMBER: US/10/432.234A  
CURRENT FILING DATE: 2003-05-22  
PRIOR APPLICATION NUMBER: US 60/252767  
PRIOR FILING DATE: 2000-11-22  
NUMBER OF SEQ ID NOS: 574  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 250  
LENGTH: 10

```

; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-10-432-234A-250
Query Match
Best Local Similarity 39.5%; Score 32; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPQDQ 10
DB 1 NDMPITNDQ 9

RESULT 8
US-10-155-693-29
; Sequence 29, Application US/10155693
; Publication No. US20030175876A1
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUOIAN
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/10/155,693
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US/08/837,199
; PRIOR FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 14
; TYPE: PRT
; ORGANISM: RAT
US-10-155-693-29

Query Match
Best Local Similarity 38.3%; Score 31; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PIQTDQYTTT 14
DB 4 PVQTTTATTT 13

RESULT 9
US-10-872-161-29
; Sequence 29, Application US/10872161
; Publication No. US20040235714A1
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUOIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401D
; CURRENT APPLICATION NUMBER: US/10/872,161
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/08/866,354
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; PRIOR APPLICATION NUMBER: US 08/837,199
; PRIOR FILING DATE: 1997-04-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 14
; TYPE: PRT
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; ORGANISM: RAT
US-10-872-161-29
Query Match
Best Local Similarity 38.3%; Score 31; DB 5; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PIQTDQYTTT 14
DB 4 PVQTTTATTT 13

RESULT 10
US-10-462-452-433
; Sequence 433, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 433
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-433

Query Match
Best Local Similarity 35.8%; Score 29; DB 4; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPQDQ 9
DB 1 NDVPLPTD 8

RESULT 11
US-10-601-953-561
; Sequence 561, Application US/10601953
; Publication No. US20040077540A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
; FILE REFERENCE: 02-03US
; CURRENT APPLICATION NUMBER: US/10/601,953
; PRIOR FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/392,512
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 561
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-601-953-561

Query Match
Best Local Similarity 35.8%; Score 29; DB 4; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 2 NDSP1QTD 9  
|||:|  
Db 1 NDVPLPTD 8

RESULT 12  
US-10-322-266-434  
; Sequence 434, Application US/10322266  
; Publication No. US20040115135A1  
; GENERAL INFORMATION:  
; APPLICANT: Quay, Steven C.  
; TITLE OF INVENTION: Compositions And Methods For Enhanced Mucosal Delivery Of Peptide  
; FILE REFERENCE: NPE10567  
; CURRENT APPLICATION NUMBER: US/10/322,266  
; CURRENT FILING DATE: 2002-12-17  
; NUMBER OF SEQ ID NOS: 797  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 434  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-10-322-266-434

Query Match 35.8%; Score 29; DB 4; Length 10;  
Best Local Similarity 62.5%; Pred. No. 3.6e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSP1QTD 9  
|||:|  
Db 1 NDVPLPTD 8

RESULT 13  
US-09-990-832C-108  
; Sequence 108, Application US/09990832C  
; Publication No. US20030149235A1  
; GENERAL INFORMATION:  
; APPLICANT: University Court of the University of Glasgow  
; TITLE OF INVENTION: Targeting peptides  
; FILE REFERENCE: PC/MC/JM/P11910US  
; CURRENT APPLICATION NUMBER: US/09/990,832C  
; CURRENT FILING DATE: 2003-01-27  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 108  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Targeting peptide sequence  
US-09-990-832C-108

Query Match 35.8%; Score 29; DB 3; Length 12;  
Best Local Similarity 62.5%; Pred. No. 4.4e+02;  
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPIQTDQY 11  
:|:|:|  
Db 2 TPIQSTQY 9

RESULT 14  
US-10-758-165-4  
; Sequence 4, Application US/10758165  
; Publication No. US20050196816A1  
; GENERAL INFORMATION:  
; APPLICANT: Hammerberg, Bruce  
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES  
; FILE REFERENCE: 5051-661  
; CURRENT APPLICATION NUMBER: US/10/758,165

; CURRENT FILING DATE: 2004-01-16  
; PRIOR APPLICATION NUMBER: US 60/440,472  
; PRIOR FILING DATE: 2003-01-16  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Ovis aries  
US-10-758-165-4

Query Match 35.8%; Score 29; DB 5; Length 15;  
Best Local Similarity 42.9%; Pred. No. 5.6e+02;  
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RNDSP1QTDQYTTT 14  
|||:|:|  
Db 1 RNKELMRGQHTTT 14

RESULT 15  
US-10-462-452-457  
; Sequence 457, Application US/10462452  
; Publication No. US20040037809A1  
; GENERAL INFORMATION:  
; APPLICANT: Quay, Steven  
; APPLICANT: Gupta, Mohammed Abd  
; APPLICANT: de Meireles, Jorge  
; TITLE OF INVENTION: Compositions and Methods for Enhanced  
; FILE REFERENCE: 02-02US  
; CURRENT APPLICATION NUMBER: US/10/462,452  
; CURRENT FILING DATE: 2003-06-16  
; PRIOR APPLICATION NUMBER: 60/393,066  
; PRIOR FILING DATE: 2002-06-28  
; NUMBER OF SEQ ID NOS: 790  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 457  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-462-452-457

Query Match 34.6%; Score 28; DB 4; Length 8;  
Best Local Similarity 62.5%; Pred. No. 1.9e+06;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNDSP1QTD 8  
|||:|  
Db 1 RNDVPLPT 8

Search completed: May 30, 2006, 10:24:42  
Job time : 48 secs

GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2006, 10:22:25 ; Search time 5.66667 Seconds  
(without alignments)  
29.481 Million cell updates/sec

Title: US-10-758-165A-1  
Perfect score: 81  
Sequence: 1 RNDSPITQDTQYTTTG 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 10973

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published Applications AA New:\*

- 1: /EMC\_Celerra\_SIDS3/ptodata/1/pubppaa/US09\_NEW\_PUB.pep:\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/1/pubppaa/US06\_NEW\_PUB.pep:\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/1/pubppaa/US07\_NEW\_PUB.pep:\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/1/pubppaa/US08\_NEW\_PUB.pep:\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/1/pubppaa/US09\_NEW\_PUB.pep:\*
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- 7: /EMC\_Celerra\_SIDS3/ptodata/1/pubppaa/US11\_NEW\_PUB.pep:\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/1/pubppaa/US60\_NEW\_PUB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	29.6	10	6	US-10-538-066-163
2	23	28.4	7	6	US-10-522-043-2
3	23	28.4	9	7	US-11-140-487A-1766
4	22	27.2	7	6	US-10-525-817-129
5	22	27.2	10	6	US-10-516-079-74
6	22	27.2	11	6	US-10-540-431-11
7	22	27.2	13	7	US-11-121-282-157
8	22	27.2	15	7	US-11-140-487A-2207
9	22	27.2	15	7	US-11-140-487A-2231
10	21	25.9	9	7	US-11-140-487A-1810
11	21	25.9	10	7	US-11-219-563-93
12	21	25.9	15	6	US-10-490-949-19
13	21	25.9	15	7	US-11-140-487A-2219
14	20	24.7	7	6	US-10-489-071-6
15	20	24.7	7	6	US-10-525-817-130
16	20	24.7	11	6	US-10-507-060A-2
17	20	24.7	12	7	US-11-054-072-335
18	20	24.7	12	7	US-11-054-072-335
19	20	24.7	12	7	US-11-122-986-570
20	20	24.7	14	7	US-11-176-182-52
21	20	24.7	15	7	US-11-176-182-31
22	19	23.5	7	7	US-11-023-959A-11
23	19	23.5	7	7	US-11-023-959A-14
24	19	23.5	9	6	US-10-538-066-174
25	19	23.5	10	6	US-10-516-079-64

26	19	23.5	10	6	US-10-538-066-172	Sequence 172, App
27	19	23.5	11	6	US-10-540-431-6	Sequence 6, Appli
28	19	23.5	12	1	US-09-784-950-10	Sequence 10, Appli
29	19	23.5	12	7	US-11-176-182-112	Sequence 112, App
30	19	23.5	12	7	US-11-054-072-7056	Sequence 7056, Ap
31	19	23.5	12	7	US-11-054-072-7057	Sequence 7057, Ap
32	19	23.5	12	7	US-11-054-072-7058	Sequence 7058, Ap
33	19	23.5	12	7	US-11-054-072-7059	Sequence 7059, Ap
34	19	23.5	12	7	US-11-054-072-7060	Sequence 7060, Ap
35	19	23.5	12	7	US-11-054-072-7061	Sequence 7061, Ap
36	19	23.5	12	7	US-11-054-072-7062	Sequence 7062, Ap
37	19	23.5	12	7	US-11-054-072-7063	Sequence 7063, Ap
38	19	23.5	12	7	US-11-054-072-7064	Sequence 7064, Ap
39	19	23.5	12	7	US-11-054-072-7065	Sequence 7065, Ap
40	19	23.5	12	7	US-11-054-072-7066	Sequence 7066, Ap
41	19	23.5	12	7	US-11-054-072-7067	Sequence 7067, Ap
42	19	23.5	13	7	US-11-176-182-17	Sequence 17, Appli
43	19	23.5	13	7	US-11-054-072-5136	Sequence 5136, Ap
44	19	23.5	13	7	US-11-054-072-5137	Sequence 5137, Ap
45	19	23.5	13	7	US-11-054-072-5138	Sequence 5138, Ap

#### ALIGNMENTS

```
RESULT 1
US-10-538-066-163
; Sequence 163, Application US/10538066
; Publication No. US2006094649A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE OF INVENTION: P1, peptides and Compositions
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538, 066
; PRIOR FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432, 017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 163
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-163

Query Match      29.6%; Score 24; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 65;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 DSPITQ 8
|||:|
DB      3 DSPIT 8

RESULT 2
US-10-522-043-2
; Sequence 2, Application US/10522043
; Publication No. US20060100143A1
; GENERAL INFORMATION:
; APPLICANT: Lu et al.
; TITLE OF INVENTION: Polypeptide
; FILE REFERENCE: 69856
; CURRENT APPLICATION NUMBER: US/10/522, 043
; CURRENT FILING DATE: 2005-01-19
; PRIOR APPLICATION NUMBER: PCT/GB03/04296
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 0306261.9
; PRIOR FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: 0223193.4
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p53 inhibitor peptide
US-10-522-043-2

Query Match      28.4%; Score 23; DB 6; Length 7;
Best Local Similarity 57.1%; Pred. No. 5.2e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      3 DSPICTD 9      ||||
Db      1 DGPERTD 7

RESULT 3
US-11-140-487A-1766
; Sequence 1766, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1766
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-1766

Query Match      28.4%; Score 23; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.2e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      4 SPIOTDQ 10      ||||
Db      1 SPLTTNQ 7

RESULT 4
US-10-525-817-129
; Sequence 129, Application US/10525817
; Publication No. US20060099592A1
; GENERAL INFORMATION:
; APPLICANT: Nuevolution A/S
; TITLE OF INVENTION: Enzymatic encoding
; FILE REFERENCE: P912PC00
; CURRENT APPLICATION NUMBER: US/10/525,817
; CURRENT FILING DATE: 2005-02-25
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
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```
; OTHER INFORMATION: Artificially produced
US-10-525-817-129

Query Match      27.2%; Score 22; DB 6; Length 7;
Best Local Similarity 80.0%; Pred. No. 5.2e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 RNDSP 5      ||||
Db      2 RGDSP 6

RESULT 5
US-10-516-079-74
; Sequence 74, Application US/10516079
; Publication No. US20060088899A1
; GENERAL INFORMATION:
; APPLICANT: ALVAREZ, Vernon L.
; APPLICANT: GRIMES, Carol A.
; APPLICANT: GORDA, Matthew A.
; TITLE OF INVENTION: Combination chemotherapy with chlorotoxin
; FILE REFERENCE: 51530-5006-MO
; CURRENT APPLICATION NUMBER: US/10/516,079
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: US 60/406,033
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/384,171
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Pep21-SCXP_ANDMA sequence
US-10-516-079-74

Query Match      27.2%; Score 22; DB 6; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      8 TDQYT 12      ||||
Db      2 TDQYT 6

RESULT 6
US-10-540-431-11
; Sequence 11, Application US/10540431
; Publication No. US2006009307A1
; GENERAL INFORMATION:
; APPLICANT: Amersham Health AS
; TITLE OF INVENTION: Contrast Agents
; FILE REFERENCE: PNO273
; CURRENT APPLICATION NUMBER: US/10/540,431
; CURRENT FILING DATE: 2005-06-22
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-540-431-11

Query Match      27.2%; Score 22; DB 6; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      10 QYTTG 15      ||||
```



Db 2 QYADG 7

RESULT 7  
US-11-121-282-197  
; Sequence 197, Application US/11121282  
; Publication No. US20060094862A1  
; GENERAL INFORMATION:  
; APPLICANT: Matti Salberg  
; APPLICANT: Jan-Ingmar Flock  
; TITLE OF INVENTION: SPECIFICITY EXCHANGERS THAT REDIRECT  
; TITLE OF INVENTION: ANTIBODIES TO A PATHOGEN  
; FILE REFERENCE: TRIPEP.7AUC4CPIC  
; CURRENT APPLICATION NUMBER: US/11/121,282  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 10/372,735  
; PRIOR FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: 10/234,579  
; PRIOR FILING DATE: 2002-08-30  
; PRIOR APPLICATION NUMBER: 09/839,666  
; PRIOR FILING DATE: 2001-04-19  
; PRIOR APPLICATION NUMBER: 09/532,106  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 09/664,945  
; PRIOR FILING DATE: 2000-09-19  
; PRIOR APPLICATION NUMBER: 09/246,258  
; PRIOR FILING DATE: 1999-02-08  
; NUMBER OF SEQ ID NOS: 199  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 197  
; LENGTH: 13  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially Synthesized Peptides  
US-11-121-282-197

Query Match 27.2%; Score 22; DB 7; Length 13;  
Best Local Similarity 80.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNDSP 5  
|||  
Db 2 RGDSP 6

RESULT 8  
US-11-140-487A-2207  
; Sequence 2207, Application US/11140487A  
; Publication No. US20060093617A1  
; GENERAL INFORMATION:  
; APPLICANT: Innogenetics N.V.  
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi  
; FILE REFERENCE: 166  
; CURRENT APPLICATION NUMBER: US/11/140,487A  
; CURRENT FILING DATE: 2005-05-31  
; PRIOR APPLICATION NUMBER: EP 04012951.2  
; PRIOR FILING DATE: 2004-06-01  
; PRIOR APPLICATION NUMBER: EP 04447239.7  
; PRIOR FILING DATE: 2004-10-28  
; PRIOR APPLICATION NUMBER: EP 05102441.2  
; PRIOR FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: US 60/576,310  
; PRIOR FILING DATE: 2004-06-03  
; PRIOR APPLICATION NUMBER: US 60/622,782  
; PRIOR FILING DATE: 2004-10-29  
; PRIOR APPLICATION NUMBER: US 60/665,395  
; PRIOR FILING DATE: 2005-03-25  
; NUMBER OF SEQ ID NOS: 2278  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2207  
; LENGTH: 15  
; TYPE: PRT

; ORGANISM: hepatitis C virus  
US-11-140-487A-2207

Query Match 27.2%; Score 22; DB 7; Length 15;  
Best Local Similarity 66.7%; Pred. No. 2.3e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPIQTD 9  
|||  
Db 2 SPVFTD 7

RESULT 9  
US-11-140-487A-2231  
; Sequence 2231, Application US/11140487A  
; Publication No. US20060093617A1  
; GENERAL INFORMATION:  
; APPLICANT: Innogenetics N.V.  
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi  
; FILE REFERENCE: 166  
; CURRENT APPLICATION NUMBER: US/11/140,487A  
; CURRENT FILING DATE: 2005-05-31  
; PRIOR APPLICATION NUMBER: EP 04012951.2  
; PRIOR FILING DATE: 2004-06-01  
; PRIOR APPLICATION NUMBER: EP 04447239.7  
; PRIOR FILING DATE: 2004-10-28  
; PRIOR APPLICATION NUMBER: US 60/576,310  
; PRIOR FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: US 60/622,782  
; PRIOR FILING DATE: 2004-10-29  
; PRIOR APPLICATION NUMBER: US 60/665,395  
; PRIOR FILING DATE: 2005-03-25  
; NUMBER OF SEQ ID NOS: 2278  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2231  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: hepatitis C virus  
US-11-140-487A-2231

Query Match 27.2%; Score 22; DB 7; Length 15;  
Best Local Similarity 66.7%; Pred. No. 2.3e+02;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPIQTD 9  
|||  
Db 10 SPVFTD 15

RESULT 10  
US-11-140-487A-1810  
; Sequence 1810, Application US/11140487A  
; Publication No. US20060093617A1  
; GENERAL INFORMATION:  
; APPLICANT: Innogenetics N.V.  
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi  
; FILE REFERENCE: 166  
; CURRENT APPLICATION NUMBER: US/11/140,487A  
; CURRENT FILING DATE: 2005-05-31  
; PRIOR APPLICATION NUMBER: EP 04012951.2  
; PRIOR FILING DATE: 2004-06-01  
; PRIOR APPLICATION NUMBER: EP 04447239.7  
; PRIOR FILING DATE: 2004-10-28  
; PRIOR APPLICATION NUMBER: EP 05102441.2  
; PRIOR FILING DATE: 2005-03-25  
; PRIOR APPLICATION NUMBER: US 60/576,310  
; PRIOR FILING DATE: 2004-06-03  
; PRIOR APPLICATION NUMBER: US 60/622,782  
; PRIOR FILING DATE: 2004-10-29  
; PRIOR APPLICATION NUMBER: US 60/665,395  
; PRIOR FILING DATE: 2005-03-25

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NUMBER OF SEQ ID NOS: 2278
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1810
LENGTH: 9
TYPE: PRT
ORGANISM: hepatitis C virus
US-11-140-487A-1810
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```
Query Match      25.9%; Score 21; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.2e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      11 YTTTG 15
      ||||
Db      2 YTTTG 6
```

```
RESULT 11
US-11-219-563-93
Sequence 93, Application US/11219563
Publication No. US20060088539A1
GENERAL INFORMATION:
APPLICANT: Bander, Neil
TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
FILE REFERENCE: 13651.001 (B2L-001)
CURRENT APPLICATION NUMBER: US/11/219,563
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: PCT/US04/06586
PRIOR FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: US 10/379,838
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 10/449,379
PRIOR FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 93
LENGTH: 10
TYPE: PRT
ORGANISM: Mus musculus
US-11-219-563-93
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Query Match      25.9%; Score 21; DB 7; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      11 YTTTG 15
      ||||
Db      2 YTTTG 6
```

```
RESULT 12
US-10-490-949-19
Sequence 19, Application US/10490949
Publication No. US20060093574A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: ALBANI, Salvatore
APPLICANT: MARTINI, Alberto
TITLE OF INVENTION: METHODS FOR EPITOPE-SPECIFIC AND CYTOKINE/ANTICYTOKINE
TITLE OF INVENTION: COMBINATION IMMUNOTHERAPIES FOR MODULATION OF PATHOGENIC
FILE REFERENCE: USCD1450-2
CURRENT APPLICATION NUMBER: US/10/490,949
CURRENT FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: PCT/US02/30578
PRIOR FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US 60/339,284
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 60/325,499
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.1
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SEQ ID NO 19
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-10-490-949-19
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Query Match      25.9%; Score 21; DB 6; Length 15;
Best Local Similarity 57.1%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      9 DQYTTTG 15
      ||||
Db      2 DYQTTTG 8
```

```
RESULT 13
US-11-140-487A-2219
Sequence 2219, Application US/11140487A
Publication No. US20060093617A1
GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
FILE REFERENCE: 166
CURRENT APPLICATION NUMBER: US/11/140,487A
CURRENT FILING DATE: 2005-05-31
PRIOR APPLICATION NUMBER: EP 04012951.2
PRIOR FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: EP 04447239.7
PRIOR FILING DATE: 2004-10-28
PRIOR APPLICATION NUMBER: EP 05102441.2
PRIOR FILING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: US 60/576,310
PRIOR FILING DATE: 2004-06-03
PRIOR APPLICATION NUMBER: US 60/622,762
PRIOR FILING DATE: 2004-10-29
PRIOR APPLICATION NUMBER: US 60/665,395
PRIOR FILING DATE: 2005-03-25
NUMBER OF SEQ ID NOS: 2278
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2219
LENGTH: 15
TYPE: PRT
ORGANISM: hepatitis C virus
US-11-140-487A-2219
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Query Match      25.9%; Score 21; DB 7; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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OY      11 YTTTG 15
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Db      2 YTTTG 6
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RESULT 14
US-10-489-071-6
Sequence 6, Application US/10489071
Publication No. US20060094672A1
GENERAL INFORMATION:
APPLICANT: PASQUALINE ET AL.
TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST
TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES
FILE REFERENCE: UTSC:856US
CURRENT APPLICATION NUMBER: US/10/489,071
CURRENT FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: PCT/US02/27836
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
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FEATURE:  
OTHER INFORMATION: Synthetic Peptide  
US-10-489-071-6

Query Match 24.7%; Score 20; DB 6; Length 7;  
Best Local Similarity 42.9%; Pred. No. 5.2e+04;  
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 RNDSPQ 7  
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| | | | |  
Db 1 RMDGPVR 7

RESULT 15  
US-10-525-817-130  
; Sequence 130; Application US/10525817  
; Publication No. US20060093592A1  
; GENERAL INFORMATION:  
; APPLICANT: Nuevolution A/S  
; TITLE OF INVENTION: Enzymatic encoding  
; FILE REFERENCE: P912PC00  
; CURRENT APPLICATION NUMBER: US/10/525,817  
; CURRENT FILING DATE: 2005-02-25  
; NUMBER OF SEQ ID NOS: 165  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 130  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificially produced  
US-10-525-817-130

Query Match 24.7%; Score 20; DB 6; Length 7;  
Best Local Similarity 80.0%; Pred. No. 5.2e+04;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 RNDSP 5  
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Db 2 RADSP 6

Search completed: May 30, 2006, 10:25:04  
Job time : 5.66667 secs

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GenCore version 5.1.8  
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## OM protein - protein search, using sw model

Run on: May 30, 2006, 09:59:16 ; Search time 20.3333 Seconds

(without alignments)  
64.572 Million cell updates/sec

Title: US-10-758-165A-1

Perfect score: 81

Sequence: 1 RNDSPIDTDQYTTTG 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

249102

Minimum DB seq length: 0  
Maximum DB seq length: 15Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

1: /EMC\_Celerra\_SIDS3/prodata/2/iaa/5 COMB.pep.\*  
2: /EMC\_Celerra\_SIDS3/prodata/2/iaa/6 COMB.pep.\*  
3: /EMC\_Celerra\_SIDS3/prodata/2/iaa/7 COMB.pep.\*  
4: /EMC\_Celerra\_SIDS3/prodata/2/iaa/H COMB.pep.\*  
5: /EMC\_Celerra\_SIDS3/prodata/2/iaa/PCUS COMB.pep.\*  
6: /EMC\_Celerra\_SIDS3/prodata/2/iaa/RE COMB.pep.\*  
7: /EMC\_Celerra\_SIDS3/prodata/2/iaa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	39.5	13	7	5223254-6 Patent No. 5223254
2	31	38.3	14	2	US-08-837-199A-29 Sequence 29, Appl
3	28.5	35.2	15	3	US-09-641-528B-48206 Sequence 48206, A
4	28	34.6	9	3	US-09-641-528B-5634 Sequence 5634, Ap
5	28	34.6	9	3	US-09-641-528B-10412 Sequence 10412, A
6	28	34.6	9	3	US-09-641-528B-35442 Sequence 35442, A
7	28	34.6	9	3	US-09-641-528B-42435 Sequence 42435, A
8	28	34.6	9	3	US-09-641-528B-51014 Sequence 51014, A
9	28	34.6	10	3	US-09-641-528B-5507 Sequence 5507, Ap
10	28	34.6	10	3	US-09-641-528B-10417 Sequence 10417, A
11	28	34.6	10	3	US-09-641-528B-35452 Sequence 35452, A
12	28	34.6	10	3	US-09-641-528B-42443 Sequence 42443, A
13	28	34.6	11	3	US-09-641-528B-5635 Sequence 5635, Ap
14	28	34.6	11	3	US-09-641-528B-10352 Sequence 10352, A
15	28	34.6	11	3	US-09-641-528B-15263 Sequence 35263, A
16	28	34.6	11	3	US-09-641-528B-42319 Sequence 42319, A
17	28	34.6	11	3	US-09-641-528B-42319 Sequence 42319, A
18	28	34.6	15	3	US-09-641-528B-47375 Sequence 47375, A
19	28	34.6	15	3	US-09-641-528B-50683 Sequence 50683, A
20	27	33.3	9	2	US-09-341-982-75 Sequence 75, Appl
21	27	33.3	12	1	US-08-479-233-8 Sequence 8, Appl
22	27	33.3	12	5	PCR-US93-00643-8 Sequence 8, Appl
23	27	33.3	15	1	US-08-209-525-50 Sequence 50, Appl
24	26	32.1	9	3	US-09-914-259-161 Sequence 161, App
25	26	32.1	9	3	US-09-641-528B-4318 Sequence 4318, Ap
26	26	32.1	9	3	US-09-641-528B-50956 Sequence 50956, A
27	26	32.1	10	3	US-09-641-528B-4238 Sequence 4238, Ap

## ALIGNMENTS

27	26	32.1	11	3	US-09-641-528B-4319	Sequence 4319, Ap
28	26	32.1	12	1	US-08-423-441-4	Sequence 4, Appl
29	26	32.1	12	2	US-09-514-739-5	Sequence 5, Appl
30	26	32.1	12	2	US-09-517-866-13	Sequence 13, Appl
31	26	32.1	12	3	US-10-279-991A-13	Sequence 1, Appl
32	26	32.1	15	2	US-10-378-707-1	Sequence 50625, A
33	26	32.1	15	3	US-09-641-528B-50625	Sequence 4, Appl
34	25	30.9	8	3	US-08-413-708B-4	Sequence 10393, A
35	25	30.9	8	3	US-09-641-528B-10393	Sequence 35388, A
36	25	30.9	8	3	US-09-641-528B-35388	Sequence 42396, A
37	25	30.9	9	3	US-09-641-528B-42396	Sequence 5590, Ap
38	25	30.9	11	1	US-09-641-528B-5590	Sequence 2, Appl
39	25	30.9	11	1	US-08-077-939-2	Sequence 2, Appl
40	25	30.9	11	1	US-08-461-559-2	Sequence 24, Appl
41	25	30.9	11	1	US-07-949-812-24	Sequence 2, Appl
42	25	30.9	11	1	US-08-461-621-2	Sequence 2, Appl
43	25	30.9	11	1	US-08-465-314-2	Sequence 5591, Ap
44	25	30.9	11	3	US-09-641-528B-5591	Sequence 14203, A
45	25	30.9	11	3	US-09-641-528B-14203	

RESULT 1  
5223254-6  
Patent No. 5223254  
APPLICANT: PARADISO, PETER R.; HILDRETH, STEPHEN W.; HU, BRADA T.; MARTIN-GALLARDO, ANTONIA; ARUMUGHAM, RASAPPA  
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES  
NUMBER OF SEQUENCES: 17  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/247,017  
FILING DATE: 20-SEP-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 102,180  
FILING DATE: 29-SEP-1987  
SEQ ID NO: 6:  
LENGTH: 13  
5223254-6  
Query Match 39.5%; Score 32; DB 7; Length 13;  
Best local similarity 66.7%; Pred. No. 36;  
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 NDSPIDTDQ 10  
DB 2 NDMPITNDQ 10  
RESULT 2  
US-08-837-199A-29  
Sequence 29, Application US/08837199A  
Patent No. 6455277  
GENERAL INFORMATION:  
APPLICANT: FOX, GARY M.  
APPLICANT: JING, SHUQIAN  
APPLICANT: WEN, DUANZHI  
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPIC FACTOR RECEPTOR  
FILE REFERENCE: A-401C  
CURRENT APPLICATION NUMBER: US/08/837,199A  
CURRENT FILING DATE: 1997-04-14  
PRIOR APPLICATION NUMBER: US 60/015,907  
PRIOR FILING DATE: 1996-04-22  
PRIOR APPLICATION NUMBER: US 60/017,221  
PRIOR FILING DATE: 1996-05-09  
NUMBER OF SEQ ID NOS: 47  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 29  
LENGTH: 14  
TYPE: PRT  
ORGANISM: RAT  
US-08-837-199A-29

Query Match 38.3%; Score 31; DB 2; Length 14;  
Best Local Similarity 60.0%; Pred. No. 58;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 IOTDOYTTT 14  
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Db 4 PVOTTTATTT 13

RESULT 3  
US-09-641-528B-48206

; Sequence 48206, Application US/09641528B  
; Patent No. 7026443  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Grey, Howard  
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
; FILE REFERENCE: 2060.0100001  
; CURRENT APPLICATION NUMBER: US/09/641,528B  
; PRIOR FILING DATE: 2000-08-15  
; PRIOR APPLICATION NUMBER: US 60/172,705  
; PRIOR FILING DATE: 1999-12-10  
; NUMBER OF SEQ ID NOS: 51505  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 48206  
; LENGTH: 15  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528B-48206

Query Match 35.2%; Score 28.5; DB 3; Length 15;  
Best Local Similarity 46.2%; Pred. No. 1.7e+02;  
Matches 6; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

OY 2 NDSPIOT-DOYTT 13  
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Db 3 NVSEVETVNEXYNT 15

RESULT 4  
US-09-641-528B-5634

; Sequence 5634, Application US/09641528B  
; Patent No. 7026443  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Grey, Howard  
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
; FILE REFERENCE: 2060.0100001  
; CURRENT APPLICATION NUMBER: US/09/641,528B  
; PRIOR FILING DATE: 2000-08-15  
; PRIOR APPLICATION NUMBER: US 60/172,705  
; PRIOR FILING DATE: 1999-12-10  
; NUMBER OF SEQ ID NOS: 51505  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5634  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus

## US-09-641-528B-5634

Query Match 34.6%; Score 28; DB 3; Length 9;  
Best Local Similarity 50.0%; Pred. No. 5e+05;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 IOTDOYTT 13  
: |||: |||  
Db 2 VSTDEYVT 9

RESULT 5  
US-09-641-528B-10412

; Sequence 10412, Application US/09641528B  
; Patent No. 7026443  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Grey, Howard  
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
; FILE REFERENCE: 2060.0100001  
; CURRENT APPLICATION NUMBER: US/09/641,528B  
; PRIOR FILING DATE: 2000-08-15  
; PRIOR APPLICATION NUMBER: US 60/172,705  
; PRIOR FILING DATE: 1999-12-10  
; NUMBER OF SEQ ID NOS: 51505  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10412  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus  
US-09-641-528B-10412

Query Match 34.6%; Score 28; DB 3; Length 9;  
Best Local Similarity 50.0%; Pred. No. 5e+05;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 IOTDOYTT 13  
: |||: |||  
Db 1 VSTDEYVT 8

RESULT 6  
US-09-641-528B-35442

; Sequence 35442, Application US/09641528B  
; Patent No. 7026443  
; GENERAL INFORMATION:  
; APPLICANT: Sette, Alessandro  
; APPLICANT: Sidney, John  
; APPLICANT: Southwood, Scott  
; APPLICANT: Chesnut, Robert  
; APPLICANT: Celis, Esteban  
; APPLICANT: Grey, Howard  
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS  
; FILE REFERENCE: 2060.0100001  
; CURRENT APPLICATION NUMBER: US/09/641,528B  
; PRIOR FILING DATE: 2000-08-15  
; PRIOR APPLICATION NUMBER: US 60/172,705  
; PRIOR FILING DATE: 1999-12-10  
; NUMBER OF SEQ ID NOS: 51505  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35442  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus

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; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
; US-09-641-528B-35442
Query Match          34.6%; Score 28; DB 3; Length 9;
Best Local Similarity 50.0%; Pred. No. 5e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      6 IQTDOYTT 13
       : ||: ||
Db      1 VSTDENVY 8

RESULT 7
US-09-641-528B-42435
; Sequence 42435, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641.528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172.705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42435
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
; US-09-641-528B-42435
Query Match          34.6%; Score 28; DB 3; Length 9;
Best Local Similarity 50.0%; Pred. No. 5e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      6 IQTDOYTT 13
       : ||: ||
Db      1 VSTDENVY 8

RESULT 8
US-09-641-528B-51014
; Sequence 51014, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641.528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172.705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51014
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
; US-09-641-528B-51014
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Best Local Similarity 50.0%; Pred. No. 5e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      6 IQTDOYTT 13
       : ||: ||
Db      1 VSTDENVY 8

RESULT 9
US-09-641-528B-5507
; Sequence 5507, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641.528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172.705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5507
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
; US-09-641-528B-5507
Query Match          34.6%; Score 28; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      6 IQTDOYTT 13
       : ||: ||
Db      3 VSTDENVY 10

RESULT 10
US-09-641-528B-10417
; Sequence 10417, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641.528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172.705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10417
; LENGTH: 10
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-10417

Query Match          34.6%; Score 28; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 IQTDQYTT 13
   : ||: ||
Db 2 VSTDENVVT 9

RESULT 11
US-09-641-528B-35452
; Sequence 35452, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Eteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641.528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35452
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-35452

Query Match          34.6%; Score 28; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 IQTDQYTT 13
   : ||: ||
Db 2 VSTDENVVT 9

RESULT 12
US-09-641-528B-42443
; Sequence 42443, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Eteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641.528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42443
; LENGTH: 10
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-42443

Query Match          34.6%; Score 28; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 IQTDQYTT 13
   : ||: ||
Db 2 VSTDENVVT 9

RESULT 13
US-09-641-528B-5635
; Sequence 5635, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Eteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641.528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5635
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-5635

Query Match          34.6%; Score 28; DB 3; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 IQTDQYTT 13
   : ||: ||
Db 2 VSTDENVVT 9

RESULT 14
US-09-641-528B-10362
; Sequence 10362, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Eteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641.528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10362
```



```

; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-10362

Query Match      34.6%; Score 28; DB 3; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      6 IQTDOYTT 13
      : ||: ||
Db      3 VSTDEYVT 10

RESULT 15
US-09-641-528B-35263
; Sequence 35263, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Ecteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35263
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-35263

Query Match      34.6%; Score 28; DB 3; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      6 IQTDOYTT 13
      : ||: ||
Db      3 VSTDEYVT 10
```

Search completed: May 30, 2006, 11:11:07  
Job time : 21.3333 secs

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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2006, 09:58:55 ; Search time 11.6667 Seconds  
(without alignments)  
123.707 Million cell updates/sec

Title: US-10-758-165A-1  
Perfect score: 81  
Sequence: 1 RNDSP1QTDQYTTTG 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 80: \*  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	34.6	14	2	PH1306
2	26	32.1	11	2	amine oxidase (cop
3	24	29.6	14	2	porin - rice (sera
4	22	27.2	14	2	Ig heavy chain DJ
5	21	25.9	11	2	PS0259
6	21	25.9	13	2	H56046
7	20.5	25.3	13	2	547376
8	20	24.7	11	2	S04875
9	20	24.7	11	2	A26120
10	20	24.7	11	2	S05002
11	20	24.7	12	2	PH0771
12	20	24.7	13	2	PN0125
13	20	24.7	10	1	PH1347
14	19	23.5	10	1	GMR012
15	19	23.5	10	2	B60656
16	19	23.5	11	2	SS8244
17	19	23.5	13	2	B61458
18	19	23.5	13	2	A61458
19	19	23.5	14	2	PH1705
20	19	23.5	14	2	SS0900
21	19	23.5	15	2	S42741
22	19	23.5	15	2	PH1631
23	18	22.2	7	2	I48086
24	18	22.2	10	2	S43625
25	18	22.2	10	2	A61332
26	18	22.2	12	2	ES8502
27	18	22.2	12	2	A61503
28	18	22.2	13	2	A33660
29	18	22.2	13	2	PT0331

30	18	22.2	14	2	PT0232	Ig heavy chain CRD
31	18	22.2	15	2	S32677	nitrogenase cofact
32	18	22.2	15	2	PA0057	serine phosphoryla
33	18	22.2	15	2	S29485	GTP-binding protei
34	18	22.2	15	2	S72432	epoxypropan isomer
35	17	21.0	8	2	I57018	gene Cfr protein
36	17	21.0	9	2	PT0247	Ig heavy chain CRD
37	17	21.0	9	2	PL0139	carbon-monoxide de
38	17	21.0	10	2	B61512	variant surface gl
39	17	21.0	11	2	C53652	rhlR protein - pse
40	17	21.0	11	2	A29806	acidic proline-ric
41	17	21.0	11	2	S42449	antl protein - pha
42	17	21.0	12	2	S25485	transcription fact
43	17	21.0	12	2	PT0228	Ig heavy chain CDR
44	17	21.0	12	2	JU0356	cycloleucorubin -
45	17	21.0	12	2	PN0170	alcohol dehydrogen

## ALIGNMENTS

RESULT 1  
PH1306  
Ig heavy chain DJ region (clone C96-100) - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999  
C/Accession: PH1306  
R/Masserian, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.  
J. Exp. Med. 176, 1577-1581, 1992  
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph  
A/Reference number: PH1302; MUID:93094761; PMID:1460419  
A/Accession: PH1306  
A/Molecule type: DNA  
A/Residues: 1-14 <MAS>  
A/Cross-references: UNIPARC:UPI000017C253  
C/Keywords: heterotetramer; immunoglobulin

Query Match 34.6%; Score 26; DB 2; Length 14;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YTTTG 15  
DB 6 YTTTG 10

RESULT 2  
S71304  
amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragment)  
C/Species: Aspergillus niger  
C/Date: 12-Feb-1998 #sequence\_revision 01-May-1998 #text\_change 09-Jul-2004  
C/Accession: S71304  
R/Firebort, I.; Tamaki, H.; Ishida, H.; Pec, P.; Luhova, L.; Tauno, H.; Halata, M.; Asano  
Eur. J. Biochem. 237, 255-265, 1996  
A/Title: Two distinct quinoprotein amine oxidases are induced by n-butylamine in the myc  
A/Reference number: S71303; MUID:96203933; PMID:8620882  
A/Accession: S71304  
A/Molecule type: protein  
A/Residues: 1-11 <PRE>  
A/Cross-references: UNIPROT:O7M504; UNIPARC:UPI000017B3B7  
C/Keywords: copper binding; monomer; oxidoreductase; quinoprotein; topaquinone

Query Match 32.1%; Score 26; DB 2; Length 11;  
Best Local Similarity 62.5%; Pred. No. 1.6e+02;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSP1QTD 9  
DB 1 NDSP1ALND 8

RESULT 3  
PS0249

porin - rice (strain Nihonbare) (fragment)

C:Species: Oryza sativa (rice)  
C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 09-Jul-2004

C:Accession: PS0249

R:Taughita, A.

submitted to JIPID, April 1993

A:Reference number: PS0206

A:Accession: PS0249

A:Molecule type: protein

A:Residues: 1-14 <TSU>

A:Cross-references: UNIPROT:Q7M1U8; UNIPARC:UPI000017B118

A:Experimental source: callus

Query Match 29.6%; Score 24; DB 2; Length 14;  
Best Local Similarity 50.0%; Pred. No. 4.8e+02;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 8 TDQYTTG 15  
| | | | |

Db 5 TDDHTANG 12

#### RESULT 4

PH1305

IG heavy chain DJ region (clone C85-1B) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C:Accession: PH1305

R:Maeserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A:Reference number: PH1302; MUID:93094761; PMID:1460419

A:Accession: PH1305

A:Molecule type: DNA

A:Residues: 1-14 <WAS>

A:Cross-references: UNIPARC:UPI000017C252

C:Keywords: heterotetramer; immunoglobulin

Query Match 27.2%; Score 22; DB 2; Length 14;  
Best Local Similarity 62.5%; Pred. No. 1.1e+03;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 IQTQYTT 13  
| | | | |

Db 2 ILTGYYT 9

#### RESULT 5

PS0259

39K protease 3225 - rice (strain Nihonbare) (fragment)

C:Species: Oryza sativa (rice)

C:Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 11-Apr-1995

C:Accession: PS0259

R:Taughita, A.; Kamo, M.

submitted to JIPID, April 1993

A:Reference number: PS0209

A:Accession: PS0259

A:Molecule type: protein

A:Residues: 1-11 <TSU>

A:Cross-references: UNIPARC:UPI000017B102

A:Experimental source: callus

C:Comment: molecular weight 39K, pI 5.7.

Query Match 25.9%; Score 21; DB 2; Length 11;  
Best Local Similarity 57.1%; Pred. No. 1.3e+03;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 DSPIQTD 9  
| | | | |

Db 5 DGPVAD 11

#### RESULT 6

H56046

urinary tract stone matrix protein 10, 42K - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 12-Apr-1995 #sequence\_revision 12-Apr-1995 #text\_change 09-Jul-2004

C:Accession: H56046

R:Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.

submitted to the Protein Sequence Database, February 1995

A:Description: Isolation, characterization and sequence of stone proteins.

A:Reference number: A56046

A:Accession: H56046

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <BIN>

A:Cross-references: UNIPROT:Q7M4P7; UNIPARC:UPI000017C406

Query Match 25.9%; Score 21; DB 2; Length 13;  
Best Local Similarity 50.0%; Pred. No. 1.5e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 NDSPIQTD 9  
| | | | |

Db 6 NDLAATD 13

#### RESULT 7

S47376

T-cell antigen receptor VT junction beta chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999

C:Accession: S47376

R:Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A\*0201 restricted recognition of influenza A is dominated by T cell

A:Reference number: S47355

A:Accession: S47376

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-13 <LEH>

A:Cross-references: UNIPARC:UPI0000116687; EMBL:Z35702; NID:G527497; PIDN:CAAB4771.1; PIR

C:Keywords: T-cell receptor

Query Match 25.3%; Score 20.5; DB 2; Length 13;  
Best Local Similarity 66.7%; Pred. No. 1.9e+03;

Matches 6; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 4 SPIQTD-QY 11  
| | | | |

Db 4 SPRSTDTQY 12

#### RESULT 8

S04875

nifs protein - Bradyrhizobium japonicum (fragment)

C:Species: Bradyrhizobium japonicum

C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 09-Jul-2004

C:Accession: S04875

R:Belong, S.

submitted to the EMBL Data Library, December 1988

A:Reference number: S04873

A:Accession: S04875

A:Molecule type: DNA

A:Residues: 1-11 <EBE>

A:Cross-references: UNIPROT:P37030; UNIPARC:UPI000016E719; EMBL:X13691; NID:G39544; PIDN

C:Genetics:

A:Gene: nifs

A:Start codon: GTG

Query Match 24.7%; Score 20; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 1.9e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 NDSPIQTD 9  
| | | | |

Db 4 NRAP1YLD 11

# RESULT 9

A26120

6-phosphofructokinase (EC 2.7.1.11) - pig roundworm (fragment)  
N:Alternate names: phosphofructokinase; phosphohexokinase

C:Species: Ascaris suum (pig roundworm)  
C:Date: 15-Dec-1988 #sequence\_revision 15-Dec-1988 #text\_change 09-Jul-2004

C:Accession: A26120

R:Kulkarni, G.; Rao, G.S.J.; Srinivasan, N.G.; Hofer, H.W.; Yuan, P.M.; Harrie, B.G.

J. Biol. Chem. 262, 32-34, 1987

A:Title: Ascaris suum phosphofructokinase. Phosphorylation by protein kinase and sequenc

A:Reference number: A26120; MUID:87083467; PMID:3025208

A:Accession: A26120

A:Molecule type: protein

A:Residues: 1-11 <KUL>

A:Cross-references: UNIPROT:Q7M4J2; UNIPARC:UPI000017B699

C:Keywords: glycolysis; phosphotransferase

Query Match 24.7%; Score 20; DB 2; Length 11;

Best Local Similarity 50.0%; Pred. No. 1.9e+03;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RNDSP1QF 8

Db 4 RSDSIVPT 11

# RESULT 10

S05002

corazonin - American cockroach

C:Species: Periplaneta americana (American cockroach)

C:Date: 07-Sep-1990 #sequence\_revision 09-Apr-1998 #text\_change 09-Jul-2004

C:Accession: S05002

R:Venestra, J.A.

FEBS Lett. 250, 231-234, 1989

A:Title: Isolation and structure of corazonin, a cardioactive peptide from the american

A:Reference number: S05002; MUID:89325572; PMID:2753132

A:Accession: S05002

A:Molecule type: protein

A:Residues: 1-11 <VEE>

A:Cross-references: UNIPROT:P11496; UNIPARC:UPI0000127F28

C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:1/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 24.7%; Score 20; DB 2; Length 11;

Best Local Similarity 66.7%; Pred. No. 1.9e+03;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 QTDQYT 12

Db 1 QTFQYS 6

# RESULT 11

PH0771

T-cell receptor beta chain (PE5.1.1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 05-Nov-1999

C:Accession: PH0771

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex-  
allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0771

A:Molecule type: mRNA

A:Residues: 1-12 <CNS>

A:Cross-references: UNIPARC:UPI0000115FBE; EMBL:X60865; NID:953624; PIDN:CAA43255.1; PID  
A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match 24.7%; Score 20; DB 2; Length 12;

Best Local Similarity 50.0%; Pred. No. 2.1e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 SPIQTDQY 11

Db 3 SSFOYEQY 10

# RESULT 12

PN0125

serine proteinase (EC 3.4.21.-) - Actinomyces sp. (fragment)

C:Species: Actinomyces sp.

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004

C:Accession: PN0125

R:Mosolova, O.V.; Rudenskaya, G.N.; Stepanov, V.M.; Khodova, O.M.; Tsaplina, I.A.

Biohimia 52, 414-422, 1987

A:Title: Glu, Asp-specific proteinase from Actinomyces.

A:Reference number: PN0125

A:Accession: PN0125

A:Molecule type: protein

A:Residues: 1-13 <MOS>

A:Cross-references: UNIPROT:Q7M107; UNIPARC:UPI000017AD24

A>Note: article in Russian with English abstract

C:Keywords: hydrolase; serine proteinase

Query Match 24.7%; Score 20; DB 2; Length 13;

Best Local Similarity 62.5%; Pred. No. 2.3e+03;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 SPIQTDQY 11

Db 1 SVIGTDVY 8

# RESULT 13

PH1347

Ig heavy chain DJ region (clone C100-103A) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 07-May-1999

C:Accession: PH1347

R:Wasserman, R.; Gallil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type DH joining in young children with B precursor lymph

A:Reference number: PH1302; MUID:93094761; PMID:1460419

A:Accession: PH1347

A:Molecule type: DNA

A:Residues: 1-14 <MAS>

A:Cross-references: UNIPARC:UPI000017C21C

C:Keywords: heterotrimer; immunoglobulin

Query Match 24.7%; Score 20; DB 2; Length 14;

Best Local Similarity 42.9%; Pred. No. 2.5e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 9 DQYTTTG 15

Db 4 EDPLTTG 10

# RESULT 14

GMR012

leucosulfakinin-II - Madeira cockroach

N:Alternate names: LSK-II

C:Species: Leucophaea maderae (Madeira cockroach)

C:Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004

C:Accession: A26335

R:Nachman, R.J.; Holman, G.M.; Cook, B.J.; Haddon, W.F.; Ling, N.

Biochem. Biophys. Res. Commun. 140, 357-364, 1986

A:Title: Leucosulfakinin-II, a blocked sulfated insect neuropeptide with homology to cho

A:Reference number: A26335; MUID:87048769; PMID:3778455

A:Accession: A26335

A:Molecule type: protein  
A:Residues: 1-10 <NAC  
A:Cross-references: UNIPROT:P09039, UNIPARC:UPI000012B961  
C:Comment: This peptide was isolated from head extracts. It stimulates muscle contractile  
C:Superfamily: gastrin  
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; sulfoprotein  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:5/Binding site: sulfate (Tyr) (covalent) #status experimental  
F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 23.5%; Score 19; DB 1; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 QTDQY 11  
|:|  
1 QSDPY 5

## RESULT 15

B60656  
leucosulfakinin II, non-sulfated - American cockroach  
C:Species: Periplaneta americana (American cockroach)  
C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 09-Jul-2004  
C:Accession: B60656  
R:Veensstra, J.A.  
Neuropeptides 14, 145-149, 1989  
A:Title: Isolation and structure of two gastrin/CK-like neuropeptides from the American  
A:Reference number: A60656; MUID:90137190; PMID:2615921  
A:Accession: B60656  
A:Molecule type: protein  
A:Residues: 1-10 <VEE>  
A:Cross-references: UNIPROT:P09039, UNIPARC:UPI000012B961  
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 23.5%; Score 19; DB 2; Length 10;  
Best Local Similarity 60.0%; Pred. No. 2.6e+03;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 QTDQY 11  
|:|  
1 QSDPY 5

Search completed: May 30, 2006, 10:13:21  
Job time : 12 secs

GenCore version 5.1.8  
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OM protein - protein search, using sw model

Run on: May 30, 2006, 09:59:07 ; Search time 67.3333 Seconds  
(without alignments)  
206.068 Million cell updates/sec

Title: us-10-758-165a-1  
Perfect score: 81  
Sequence: 1 RNDSP1QTDQYTTTG 15

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 8966

Minimum DB seq length: 0  
Maximum DB seq length: 15

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 7.2: \*  
1: uniprot\_sprot: \*  
2: uniprot\_trembl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	26	32.1	11 2 Q7M504 ASPNG	Q7M504 aspergillus
2	24	29.6	13 2 Q2WDG6_FICBY	Q2WDG6 ficedula hy
3	24	29.6	13 2 Q2WDH5_FICAL	Q2WDH5 ficedula al
4	24	29.6	13 2 Q804K2_FICPA	Q804K2 ficedula pa
5	24	29.6	14 2 Q7M1U8_ORYSA	Q7M1U8 oryza sativ
6	24	29.6	15 2 Q9S929_SOYBN	Q9S929 glycine max
7	23	28.4	13 1 P1MS_LANNA	P1MS009 lamna nasus
8	23	28.4	15 1 OLP_TOBAC	P80781 nicotiana t
9	22	27.2	9 2 Q9TVF1_TRYCR	Q9TVF1 trypanosoma
10	22	27.2	10 1 SC41_TITCA	P84684 titlusa camb
11	22	27.2	14 2 Q71GS6_9HYME	Q71GS6 andrena n.
12	22	27.2	14 2 Q54394_STRLI	Q54394 streptomyces
13	22	27.2	15 1 UC19_MATZE	P80625 zea mays (m
14	22	27.2	15 2 Q71GV6_9HYME	Q71GV6 andrena sim
15	22	27.2	15 2 Q71H38_9HYME	Q71H38 andrena aur
16	21	25.9	8 2 Q15893_HUMAN	Q15893 homo sapien
17	21	25.9	13 2 Q7M4P7_HUMAN	Q7M4P7 homo sapien
18	21	25.9	14 2 Q7ZC2_CVPCA	Q7ZC2 cyprinus ca
19	21	25.9	15 2 Q71GTO_9HYCA	Q71GTO andrena aff
20	20	24.7	8 2 Q71H2_YEAST	Q71H2 saccharomyc
21	20	24.7	10 1 DDP2_BOVIN	P11180 bos taurus
22	20	24.7	11 1 COR2_PERAM	P11496 periplaneta
23	20	24.7	11 1 CWP08_LYCES	P80805 lycopersico
24	20	24.7	11 2 Q7M4J2_ASCSU	Q7M4J2 ascaris suu
25	20	24.7	11 2 Q9TRR7_RABIT	Q9TRR7 cycloclagus
26	20	24.7	11 2 Q6SR12_CVHSA	Q6SR12 sars corona
27	20	24.7	12 2 Q6SR16_CVHSA	Q6SR16 sars corona
28	20	24.7	12 2 Q6SRJ0_CVHSA	Q6SRJ0 sars corona
29	20	24.7	12 2 Q6SRJ4_CVHSA	Q6SRJ4 sars corona
30	20	24.7	12 2 Q6SRJ8_CVHSA	Q6SRJ8 sars corona
31	20	24.7	12 2 Q6SRK2_CVHSA	Q6SRK2 sars corona

32	20	24.7	12 2 Q6SRK6_CVHSA	Q6SRK6 sars corona
33	20	24.7	12 2 Q6SRJ0_CVHSA	Q6SRJ0 sars corona
34	20	24.7	12 2 Q6SRJ4_CVHSA	Q6SRJ4 sars corona
35	20	24.7	12 2 Q6SRJ8_CVHSA	Q6SRJ8 sars corona
36	20	24.7	12 2 Q6SRM2_CVHSA	Q6SRM2 sars corona
37	20	24.7	12 2 Q6SRM6_CVHSA	Q6SRM6 sars corona
38	20	24.7	12 2 Q6SRN0_CVHSA	Q6SRN0 sars corona
39	20	24.7	12 2 Q6SRN4_CVHSA	Q6SRN4 sars corona
40	20	24.7	12 2 Q6SRN8_CVHSA	Q6SRN8 sars corona
41	20	24.7	12 2 Q6SRP2_CVHSA	Q6SRP2 sars corona
42	20	24.7	12 2 Q6SRP6_CVHSA	Q6SRP6 sars corona
43	20	24.7	12 2 Q6SRQ0_CVHSA	Q6SRQ0 sars corona
44	20	24.7	13 1 EP65_HUMAN	P54963 homo sapien
45	20	24.7	13 2 Q7M107_9ACTO	Q7M107 actinomyces

## ALIGNMENTS

RESULT 1  
Q7M504 ASPNG PRELIMINARY; PRT; 11 AA.  
AC Q7M504;  
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.  
DT 15-DEC-2003, sequence version 1.  
DT 07-FEB-2006, entry version 8.  
DE Amine oxidase (copper-containing) (EC 1.4.3.6) II (Fragment).  
OS Aspergillus niger.  
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;  
OC Eukaryotes; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.  
OX NCBI\_TaxID=5061;  
RN [1]  
RP PROTEIN SEQUENCE.  
RX MEDLINE=96203933; PubMed=8620882;  
RA Firebort I., Tamaki H., Ishida H., Pec P., Luhova L., Tsuno H.,  
RA Halata M., Amano Y., Kato Y., Matsushita K., Toyama H., Kumagai H.,  
RA Adachi O.;  
RT "Two distinct quinoprotein amine oxidases are induced by n-butylamine  
in the mycelia of Aspergillus niger AKU 3302. Purification,  
RT characterization, cDNA cloning and sequencing.";  
RL Eur. J. Biochem. 237:255-265(1996).  
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CC  
CC  
CC PIR: S71304; S71304.  
DR GO: GO:0008131; F:amine oxidase activity; IEA.  
FT NON\_TER 1 1  
FT NON\_TER 11 11  
SQ SEQUENCE 11 AA; 1158 MW; 21BBBFDCA4472DC7 CRC64;  
Query Match 32.1%; Score 26; DB 2; Length 11;  
Best Local Similarity 62.5%; Pred. No. 1.7e+03;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 2 NDSPIQTD 9  
DB 1 NDSPLAND 8  
RESULT 2  
Q2WDG6\_FICBY PRELIMINARY; PRT; 13 AA.  
AC Q2WDG6;  
DT 10-JAN-2006, integrated into UniProtKB/TrEMBL.  
DT 10-JAN-2006, sequence version 1.  
DT 07-FEB-2006, entry version 3.  
DE Aldolase B (Fragment).  
GN Name=ab;  
OS Ficedula hypoleuca (Pied flycatcher).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.  
OX NCBI\_TaxID=46689;

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RN NUCLEOTIDE SEQUENCE.
RP STRAIN=SP11, SP19, SP21, SP23, SP24, SP4, SP6, SP8, and SP9;
RX PubMed=1595661; DOI=10.1534/genetics.105.045120;
RA Borge T., Webster M.T., Anderson G., Saetre G.-P.;
RT "Contrasting Patterns of Polymorphism and Divergence on the Z
  Chromosome and Autosomes in Two Ficedula Flycatcher Species.";
RL Genetics 171:1861-1873(2005).
-----
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DR EMBL; AJ869954; CA135707.1; -; Genomic DNA.
DR EMBL; AJ869955; CA135708.1; -; Genomic DNA.
DR EMBL; AJ869956; CA135709.1; -; Genomic DNA.
DR EMBL; AJ869957; CA135710.1; -; Genomic DNA.
DR EMBL; AJ869958; CA135711.1; -; Genomic DNA.
DR EMBL; AJ869959; CA135712.1; -; Genomic DNA.
DR EMBL; AJ869960; CA135713.1; -; Genomic DNA.
DR EMBL; AJ869961; CA135714.1; -; Genomic DNA.
DR EMBL; AJ869962; CA135715.1; -; Genomic DNA.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1635 MW; 7D3029BDE712DEA4 CRC64;

Query March 29.6%; Score 24; DB 2; Length 13;
Best Local Similarity 45.5%; Pred. No. 4.6e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 DSP1QTDQYTT 13
Db 1 DHD1QRCQYVT 11

RESULT 3
Q2WDH5_FICAL PRELIMINARY; PRT; 13 AA.
ID Q2WDH5_FICAL
AC Q2WDH5;
DT 10-JUN-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 3.
DE Aldolase B (Fragment).
GN Name=ab;
OS Ficedula albicollis (Collared flycatcher).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=59894;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=IC10, IC2, IC3, IC4, IC5, IC6, IC7, IC8, and IC9;
RX PubMed=1595661; DOI=10.1534/genetics.105.045120;
RA Borge T., Webster M.T., Anderson G., Saetre G.-P.;
RT "Contrasting Patterns of Polymorphism and Divergence on the Z
  Chromosome and Autosomes in Two Ficedula Flycatcher Species.";
RL Genetics 171:1861-1873(2005).
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DR EMBL; AJ869945; CA135698.1; -; Genomic DNA.
DR EMBL; AJ869946; CA135699.1; -; Genomic DNA.
DR EMBL; AJ869947; CA135700.1; -; Genomic DNA.
DR EMBL; AJ869948; CA135701.1; -; Genomic DNA.
DR EMBL; AJ869949; CA135702.1; -; Genomic DNA.
DR EMBL; AJ869950; CA135703.1; -; Genomic DNA.
DR EMBL; AJ869951; CA135704.1; -; Genomic DNA.
DR EMBL; AJ869952; CA135705.1; -; Genomic DNA.
DR EMBL; AJ869944; CA135697.1; -; Genomic DNA.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1635 MW; 7D3029BDE712DEA4 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 13;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Query Match 29.6%; Score 24; DB 2; Length 13;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
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Best Local Similarity 45.5%; Pred. No. 4.6e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 DSP1QTDQYTT 13
Db 1 DHD1QRCQYVT 11

RESULT 4
Q804K2_FICPA PRELIMINARY; PRT; 13 AA.
ID Q804K2_FICPA
AC Q804K2;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, entry version 1.
DT 07-FEB-2006, entry version 8.
DE Aldolase B (Fragment).
GN Name=Aldob; Synonyms=ab;
OS Ficedula parva (Red-breasted flycatcher).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=126711;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Parv;
RA Saetre G.-P., Borge T., Lindroos K., Haavie J., Sheldon B.C.,
RA Primer C.R., Syvanen A.-C.;
RT "Sex chromosome evolution and speciation in Ficedula flycatchers.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 0:0-0(2003).
RN [2]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Parv;
RX PubMed=1595661; DOI=10.1534/genetics.105.045120;
RA Borge T., Webster M.T., Anderson G., Saetre G.-P.;
RT "Contrasting Patterns of Polymorphism and Divergence on the Z
  Chromosome and Autosomes in Two Ficedula Flycatcher Species.";
RL Genetics 171:1861-1873(2005).
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DR EMBL; AY154343; AA017275.1; -; Genomic DNA.
DR EMBL; AJ869953; CA135706.1; -; Genomic DNA.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1635 MW; 7D3029BDE712DEA4 CRC64;

Query March 29.6%; Score 24; DB 2; Length 13;
Best Local Similarity 45.5%; Pred. No. 4.6e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 DSP1QTDQYTT 13
Db 1 DHD1QRCQYVT 11

RESULT 5
Q7M1U8_ORYSA PRELIMINARY; PRT; 14 AA.
ID Q7M1U8_ORYSA
AC Q7M1U8;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, entry version 1.
DT 07-FEB-2006, entry version 7.
DE Porin (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Euphorbiaceae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RN PROTEIN SEQUENCE.
RP Tsugita A.;
RL Submitted (APR-1993) to the PIR data bank.
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CC PIR; PS0249; PS0249.
DR Gramene; Q7MIU8; -.
FT NON_TER 1 1
CC NON_TER 14 14
SQ SEQUENCE 14 AA; 1490 MW; 83240AEOB1FAEA CRC64;

Query Match
Best Local Similarity 29.6%; Score 24; DB 2; Length 14;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 8 TDQYTTTG 15
DB 5 TDDHTANG 12

RESULT 6
O9S929_SOYBN PRELIMINARY; PRT; 15 AA.
AC O9S929;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Pyroline-5-carboxylate reductase, P5CR (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosidae; eurosoids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Glycine.
OX NCBI_TaxID=3847;
RN (1)
RP PROTEIN SEQUENCE.
RA MEDLINE=91378472; PubMed=1898034;
RA Chilson O.P., Kelly-Chilson A.E., Siegel N.R.;
RT "Pyroline-5-carboxylate reductase in soybean nodules:
RT isolation/partial primary structure/evidence for isozymes.";
RL Arch. Biochem. Biophys. 288:350-357 (1991).
CC -----
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CC -----
FT NON_TER 15
SQ SEQUENCE 15 AA; 1715 MW; D9821F773F3DF524 CRC64;

Query Match
Best Local Similarity 29.6%; Score 24; DB 2; Length 15;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 PIQTQDQYT 12
DB 5 PIPEASYT 12

RESULT 7
ID PLMS_LAMNA STANDARD; PRT; 13 AA.
AC P83009;
DT 29-MAR-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Phospholemman-like protein (PLMS) (Fragment).
OS Lama naus (Potoridae) (Squalus naus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes; Alopiidae;
OC Lama.
OX NCBI_TaxID=7849;
RN (1)
RP PROTEIN SEQUENCE.
RA TISSUE=Rectal gland;
RA MEDLINE=21534268; PubMed=11676495; DOI=10.1006/dbrc.2001.5826;
RA Schumanns Stekhoven F.M.A.H., Plik G., Wendelaar Bonga S.E.;
RT "N-terminal sequences of small ion channels in rectal glands of
```

```
RT sharks: a biochemical hallmark for classification and phylogeny?";
RL Biochem. Biophys. Res. Commun. 288:670-675(2001).
CC -1- FUNCTION: Induces a hyperpolarization-activated chloride current
CC when expressed in Xenopus oocytes. May have a functional role in
CC muscle contraction.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Mitochondrial
CC membrane.
CC -1- PTM: Major plasma membrane substrate for camp-dependent protein
CC kinase (PK-A) and protein kinase C (PK-C) in several different
CC tissues. Phosphorylated in response to insulin and adrenergic
CC stimulation (By similarity).
CC -1- SIMILARITY: Belongs to the FXVD family.
CC -----
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CC -----
DR GO; GO:0005792; C:mitosome; IDA.
DR InterPro; IPR000272; FXVD.
DR PROSITE; PS01310; FXVD. PARTIAL.
KW Chloride; Chloride channel; Direct protein sequencing;
KW Endoplasmic reticulum; Ion transport; Ionic channel; Membrane;
KW Microsome; Phosphorylation; Transmembrane; Transport.
FT CHAIN 1 >13 /FTid=PRO_0000148181.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1542 MW; 081373C69724A444 CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 1; Length 13;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 NDSPIQTQDQYT 12
DB 2 SDVPPNDRFT 12

RESULT 8
ID OLP_TOBAC STANDARD; PRT; 15 AA.
AC P80781;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 11-OCT-2005, sequence version 1.
DT 07-MAR-2006, entry version 5.
DE Osmotin-like protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN (1)
RP PROTEIN SEQUENCE. AND SUBCELLULAR LOCATION.
RA MEDLINE=97332671; PubMed=9188482; DOI=10.1074/jbc.272.25.15841;
RA Robertson D., Mitchell G.P., Gilroy J.B., Gerrish C., Botwell G.P.,
RA Slabas A.R.;
RT "differential extraction and protein sequencing reveals major
RT differences in patterns of primary cell wall proteins from plants.";
RL J. Biol. Chem. 272:15841-15848(1997).
CC -1- SUBCELLULAR LOCATION: Cell wall.
CC -1- SIMILARITY: Belongs to the thaumatin family.
CC -----
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CC -----
DR InterPro; IPR001938; Thaumatin.
DR PROSITE; PS00316; THAUMATIN; PARTIAL.
KW Cell wall; Direct protein sequencing.
FT CHAIN 1 >15 /FTid=PRO_0000096233.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1744 MW; 00030D70002A376B CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 1; Length 15;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 RNDSP 5  
|:|:|  
Db 6 RNDSP 10

RESULT 9

O9TVF1\_TRYCR PRELIMINARY; PRT; 9 AA.  
ID O9TVF1\_TRYCR  
AC O9TVF1  
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.  
DT 01-MAY-2000, sequence version 1.  
DT 07-FEB-2006, entry version 10.  
DE Mucin-like protein (Fragment).  
GN Name=EMUC-19c8;  
OS Trypanosoma cruzi.  
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;  
OC Schizotrypanum.  
OX NCBI\_TaxID=5693;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STAIN=C1-Brenner;  
RX MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;  
RA Di Nola J.M., D'Oreco I., Aelund L., Sanchez D.O., Frasch A.C.;  
RT "The Trypanosoma cruzi mucin family is transcribed from hundreds of  
RT genes having hypervariable regions";  
RL J. Biol. Chem. 273:10843-10850(1998).  
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CC -----  
DR EMBL: AF036447; AAC14246.1; -, mRNA.  
FT NON\_TER 1  
SQ SEQUENCE 9 AA; 896 MW; DBA831B1B55D72D CRC64;

Query Match 27.2%; Score 22; DB 2; Length 9;  
Best Local Similarity 80.0%; Pred. No. 2.8e+06;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 YTTTG 15  
|:|:|  
Db 5 YTTTG 9

RESULT 10

SC41\_TITCA STANDARD; PRT; 10 AA.  
ID SC41\_TITCA  
AC P84684;  
DT 25-OCT-2005, integrated into UniProtKB/Swiss-Prot.  
DT 25-OCT-2005, sequence version 1.  
DT 07-FEB-2006, entry version 5.  
DE Toxin Tc41 (Fragment).  
OS Tityus cambridgei (Amazonian scorpion).  
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;  
OC Buthida; Buthoidea; Buthidae; Tityus.  
OX NCBI\_TaxID=184226;  
RN [1]  
RP PROTEIN SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS  
RP SPECTROMETRY.  
RC TISSUE=Venom;  
RX PubMed=15025998; DOI=10.1016/j.jchromb.2003.09.002;  
RA Batista C.V.F., del Pozo L., Zamudio F.Z., Contreras S., Becerril B.,  
RA Mahe E., Poeschl L.D.;  
RT "Proteomics of the venom from the Amazonian scorpion Tityus cambridgei  
RT and the role of prolines on mass spectrometry analysis of toxins.";  
RL J. Chromatogr. B 803:55-66(2004).  
CC -1- SUBCELLULAR LOCATION: Secreted protein.  
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.  
CC -1- MASS SPECTROMETRY: MW=7109.4; METHOD=Electrospray; RANGE=1-7;  
CC NOTE=Ref.1.  
CC -----  
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CC -----

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CC -----  
CC Direct protein sequencing; Toxin.  
KW CHAIN 1  
FT FT >10  
FT FT /FTID=PRO\_0000066806.  
SQ SEQUENCE 10 AA; 1151 MW; 833166AAB3D77B5A CRC64;

Query Match 27.2%; Score 22; DB 1; Length 10;  
Best Local Similarity 37.5%; Pred. No. 7.8e+03;  
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 RNDSP10T 8  
|:|:|:|  
Db 1 KDDYFVD 8

RESULT 11

O7IGS6\_9HME PRELIMINARY; PRT; 14 AA.  
ID O7IGS6\_9HME  
AC O7IGS6  
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
DT 05-JUL-2004, sequence version 1.  
DT 07-MAR-2006, entry version 8.  
DE Cytochrome oxidase subunit I (Fragment).  
OS Andrena n. sp. 'goth'.  
OC Mitochondrion.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygotha;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;  
OC Andrenidae; Andreninae; Andrena; Callandrena.  
OX NCBI\_TaxID=205171;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=96;  
RX PubMed=16343953; DOI=10.1016/j.ympev.2005.10.003;  
RA Larkin L.V., Neft U.L., Simpson B.B.;  
RT "Phylogeny of the Callandrena subgenus of Andrena (Hymenoptera:  
RT Andrenidae) based on mitochondrial and nuclear DNA data: Polyphyly and  
RT convergent evolution.";  
RL Mol. Phylogenet. Evol. 38:330-343 (2006).  
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CC -----  
DR EMBL: AF504376; AAC07723.1; -, Genomic\_DNA.  
DR GO: GO:0005739; C:mitochondrion; IEA.  
KM Mitochondrion.  
FT NON\_TER 1  
SQ SEQUENCE 14 AA; 1692 MW; 79E3B922A4E7BE5B CRC64;

Query Match 27.2%; Score 22; DB 2; Length 14;  
Best Local Similarity 57.1%; Pred. No. 1.1e+04;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDSP10T 8  
|:|:|:|  
Db 6 NEIPIMT 12

RESULT 12

O54394\_STRLI PRELIMINARY; PRT; 14 AA.  
ID O54394\_STRLI  
AC O54394  
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.  
DT 01-NOV-1996, sequence version 1.  
DT 07-FEB-2006, entry version 19.  
DE S-adenosyl-L-homocysteine hydrolase (Fragment).  
OS Streptomyces lividans.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycinae; Streptomycetaceae; Streptomycetes.  
OX NCBI\_TaxID=1916;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
CC -----  
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CC -----

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RC STRAIN=TK21;
RA Romero N.M., Mellado R.P.;
RT "Activation of the actinorhodin biosynthetic pathway in Streptomyces
RL lividans.";
CC FEMS Microbiol. Lett. 1217:79-84(1995).
CC -----
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CC -----
DR EMBL; X79814; CAA56211.1; -; Genomic DNA.
DR GO; GO:0004013; F:adenosylhomocysteinease activity; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro; IPR000043; Ad_hcy_hydrolyase.
DR Pfam; PF05221; AdoHcyase; 1.
DR HydroLase.
KW NON_TER
FT SEQUENCE 14 AA; 1725 MW; 1303D5023C485D2B CRC64;

Query Match 27.2%; Score 22; DB 2; Length 14;
Best Local Similarity 33.3%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 DSPLOTDOY 11
DB 4 EGPYKADHY 12

RESULT 13
UC19_MAIZE STANDARD; PRT; 15 AA.
AC P80625;
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 406
DE (Fragment)).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Riccardi F., Morin C., Damerval C., Hueb J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.6, its MW is: 18.4 kDa.
CC -----
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CC -----
DR Gramene; P80625; -;
DR MaizeDB; 123951; -;
KW Direct protein sequencing.
FT CHAIN <1 >15
FT FT
FT NON_TER 1
FT NON_TER 1
FT SEQUENCE 15 AA; 1672 MW; 1CF69DADA8737F9D CRC64;

Query Match 27.2%; Score 22; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 QYTTTG 15
DB 4 RYTTYG 9

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RESULT 14
ID Q71GV6_9HYME PRELIMINARY; PRT; 15 AA.
AC Q71GV6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-MAR-2006, entry version 9.
DE Cytochrome oxidase subunit I (Fragment).
OS Andrena simulata.
OC Andrena.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyrgota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Apoidea;
OC Andrenidae; Andreninae; Andrena; Callandrena.
OX NCBI_TaxID=205253;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=104;
RX PubMed=16343953; DOI=10.1016/j.ympev.2005.10.003;
RA Larkin L.V., Neft U.L., Simpson B.B.;
RT "Phylogeny of the Callandrena subgenus of Andrena (Hymenoptera:
RT Andrenidae) based on mitochondrial and nuclear DNA data: Polyphly and
RT convergent evolution.";
RL Mol. Phylogenet. Evol. 38:330-343(2006).
CC -----
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CC -----
DR EMBL; AF504361; AA007693.1; -; Genomic DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
FT SEQUENCE 15 AA; 1744 MW; 181E812922A4F3EE CRC64;

Query Match 27.2%; Score 22; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQT 8
DB 6 NEIPMT 12

RESULT 15
ID Q71H38_9HYME PRELIMINARY; PRT; 15 AA.
AC Q71H38;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-MAR-2006, entry version 9.
DE Cytochrome oxidase subunit I (Fragment).
OS Andrena auripes.
OC Andrena.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyrgota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Apoidea;
OC Andrenidae; Andreninae; Andrena; Callandrena.
OX NCBI_TaxID=205215;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=126;
RX PubMed=16343953; DOI=10.1016/j.ympev.2005.10.003;
RA Larkin L.V., Neft U.L., Simpson B.B.;
RT "Phylogeny of the Callandrena subgenus of Andrena (Hymenoptera:
RT Andrenidae) based on mitochondrial and nuclear DNA data: Polyphly and
RT convergent evolution.";
RL Mol. Phylogenet. Evol. 38:330-343(2006).
CC -----
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CC -----
DR EMBL; AF504320; AA007611.1; -; Genomic DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.

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KW Mitochondrion. 1  
FT NON TER 1  
SQ SEQUENCE 15 AA; 1776 MW; 09EE90D922A4BE59 CRC64;  
Query Match 27.2%; Score 22; DB 2; Length 15;  
Best Local Similarity 57.1%; Pred. No. 1.2e+04;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
OY 2 NDSP1QT 8  
| : | | |  
Db 6 NEIP1MT 12

Search completed: May 30, 2006, 11:10:02  
Job time : 68.3333 secs